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EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,930

EARLIER FILING DATE: 1997-07-08

EARLIER FILING DATE: 1997-08-18

EARLIER FILING DATE: 1997-08-18

EARLIER FILING DATE: 1997-08-18

EARLIER FILING DATE: 1997-08-18

EARLIER APPLICATION NUMBER: 60/055,949

EARLIER APPLICATION NUMBER: 60/055,949

EARLIER FILING DATE: 1997-08-18

EARLIER FILI
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US-09-227-357-617
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3 WMKTLQGLLDRIQAFP 18

| : |:||| |::: | 65 WAELLEGLLQRLESRP 80

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Search completed: November 10, 2004, 15:57:21 Job time : 11.1779 secs

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OM protein - protein search, using sw model

November 11, 2004, 02:43:24; Search time 53.1601 Seconds (without alignments) 146.426 Million cell updates/sec Run on:

US-10-092-750-68 118 1 ATWMKTLQGILIDRIQAPPSSPH 22

Title: Perfect score: Sequence:

1568699 seqs, 353819137 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Searched:

1568699 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_MEW_PUB.pep:*
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19: /cgn2_6/ptodata/2/pubpaa/USIOR_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 68, Appl	Sequence 46367, A	Sequence 10282, A	Sequence 108, App	Sequence 3055, Ap	Sequence 246, App	Sequence 246, App	Sequence 2238, Ap	Sequence 1037, Ap	Sequence 42581, A	Sequence 2028, Ap	Sequence 115384,	Sequence 45536, A
ID	US-10-092-750-68	US-10-282-122A-46367	US-09-815-242-10282	US-09-948-820-108	US-10-104-047-3055	US-09-981-876-246	US-09-148-545-246	US-10-264-237-2238	US-10-408-765A-1037	US-10-282-122A-42581	US-10-094-749-2028	US-10-437-963-115384	US-10-282-122A-45536
	14	15	თ	10	14	σ	10	15	16	15	14	16	15
% Query Match Length DB	22	301	403	112	113	339	339	486	486	352	139	213	299
% Query Match	100.0	44.9	43.2	42.8	42.4	42.4	42.4	42.4	42.4	41.9	40.7	40.7	40.7
Score	118	53	51	50.5	20	20	50	20	20	49.5	48	48	48
Result No.	-	7	m	4	Ŋ	9	7	œ	თ	10	11	12	13

Sequence 174132, Sequence 174132, Sequence 171903, Sequence 204400, Sequence 138270,	equence 382, equence 565, equence 779, equence 159, equence 16859	Sequence 17953, A Sequence 346804, Sequence 204192, Sequence 255172, Sequence 223390,	Sequence Sequence Sequence Sequence Sequence	5059, 103251 10325 20346 20346 178053, 128051
US-10-43' US-10-43' US-10-43' US-10-43'	US-10-109-048-382 US-10-109-048-565 US-10-109-048-765 US-10-109-048-159 US-10-437-963-16859	US-110-437-953-15295-15795-10-425-11228-1228-1228-1228-1228-1295-128-128-128-128-128-128-128-128-128-128	US-10-424-599-275 US-10-437-963-110 US-09-925-300-984 US-10-425-115-308 US-10-767-701-438 US-10-425-115-287	US-09-815-242-505 US-10-282-1223-4 US-10-330-154-54 US-10-431-953-20 US-10-437-963-20 US-10-369-493-36 US-10-3437-963-12 US-10-437-963-12 US-10-437-963-12
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## ALIGNMENTS

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100.0%; Score 118; DB 14; Length 22; 100.0%; Pred. No. 3e-11; cive 0; Mismatches 0; Indels
US-10-02-750-68

US-10-02-750-68

Sequence 68, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alpin, Unlia

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 5003-6/05000.
CURRENT APPLICATION NUMBER: US-10/092,750

CURRENT FILING DATE: 2002-03-07

PRIOR PPLILCATION NUMBER: US 60/274,526

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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RESULT 2
US-10-282-122A-46367
; Sequence 46367, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

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FRIUM THIMING DATE: 2000-10-20

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-05-26

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-11-27

PRIOR PILING DATE: 2001-12-22

RIOR PILING DATE: 2001-22-26

PRIOR PILING DATE: 2001-22-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FRAESEQ for Windows Version 4.0

SEQ ID NO 10282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MKTLOGLLDRIQAFPSSPH 22
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Best Local Similarity 63.2%;
Matches 12; Conservative (
   FILING DATE: 2000-03-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 50.0
Matches 9; Conservative
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CRGANISM: Homo sapiens
US-09-948-820-108
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034 WS/10/282,122A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT PELING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR PELING DATE: 2000-05-23

PRIOR PELING DATE: 2000-05-26

PRIOR FILING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR PELING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/24,578

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-12-22

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-09

PRIOR PELING DATE: 2001-02-16

PRIOR PELING DATE: 2001-02-16
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44.9%; Score 53; DB 15; Length 301;
Best Local Similarity 42.1%; Pred. No. 7.5;
Matches 8; Conservative 7; Mismatches 4; Indels
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Sequence 10282, Application US/09815242

Patent No. US20020061569A1

GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Zyskind, Undith W.
APPLICANT: Tawick, John D.
APPLICANT: Tawick, John D.
APPLICANT: Yamanoto, Robert T.
APPLICANT: Yamanoto, Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA, 011A
CURRENT FILING DATE: 2011-03-21

PRIOR APPLICATION NUMBER: 60/191,078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 IQTTKGLIKQLQALPAKPH 106
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Wang, Liangsu
Zamudio, Carlos
Malone, Cheryl
Haselbeck, Robert
Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Bacillus anthracis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-282-122A-46367
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Pred. No. 6.4;
0; Mismatches 6; Indels 1;
43.2%; Score 51; DB 9; Length 403; 50.0%; Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3055, Application US/10104047
Publication No. US20030236392A1
GENERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US200330236392A1e1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
                                                  5; Indels
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ni et al.
TITLE OF INVENTION: 31 Human Secreted Proteins
FILE REFERENCE: P2034P1
FILE REPERENCE: P2034P1
CURRENT APPLICATION NUMBER: US/09/948,820
CURRENT FILING DATE: 2001-09-10
PRIOR APPLICATION NUMBER: US/09/565,391
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-09
PRIOR FILING DATE: 1999-11-12
PRIOR FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 115
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 108
LENGTH: 112
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R APPLICATION NUMBER: 60/047,598
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R PAPLICATION NUMBER: 60/047,613
R R APPLICATION NUMBER: 60/047,595
R R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,596
R APPLICATION NUMBER: 60/047,612
R APPLICATION NUMBER: 60/047,612
R APPLICATION NUMBER: 60/047,612
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R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,601
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/043,580
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,568
R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/043,314
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RR FILING DATE: 1997-04-11

RR PILING DATE: 1997-04-11

RR APPLICATION NUMBER: 60/043,572

RR RILING DATE: 1997-04-11

RR PILLING DATE: 1997-04-11

RR FILING DATE: 1997-06-16
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,877
R APPLICATION NUMBER: 60/056,889
R RILING DATE: 1997-08-22
R RILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,878
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,662
R R FILING DATE: 1997-08-22
                                                                         APPLICATION NUMBER: 60/047,492
FILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
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FILING DATE: 1997-04-11
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,882
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,637
PILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/043,674
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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            PRESENTATION OF SEPTIMENT OF SE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: 1

TITLE OF INVENTION: 10 Human Secreted Proteins
FILE REFERENCE: PZ00191
CURRENT APPLICATION NUMBER: US/09/981,876
CURRENT FILING DATE: 2001-10-19
PRIOR PLING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR FILING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR PLING DATE: 1997-03-07
PRIOR PPLICATION NUMBER: 60/040,626
PRIOR PLING DATE: 1997-03-07
PRIOR PLING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 246, Application US/09981876
Patent No. US20020164669A1
GENERAL INFORMATION:
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32 TWQQALTGLLERMQTY 47
PRIOR APPLICATION NUMBER:
PRIOR FILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3055
LENGTH: 113
TYPE: PRT
CRGANISM: Homo sapiens
US-10-104-047-3055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-981-876-246
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PRIOR FILING DARE: 1997-08-22

PRIOR APPLICATION NUMBER: 60/165, 910

PRIOR FILING DARE: 1997-08-22

PRIOR STAING DARE: 1997-08-22

PRIOR PILING DARE: 1997-08-22

PRIOR PILING DARE: 1997-08-22

PRIOR PILING DARE: 1997-08-22

PRIOR PILING DARE: 1997-08-23

PRIOR PAPLICATION NUMBER: 60/04, 59

PRIOR PAPLICATION NUMBER: 60/04, 59

PRIOR PAPLICATION NUMBER: 60/04, 59

PRIOR PAPLICATION NUMBER: 60/05, 64

PRIOR PAPLICATION NUMBER: 60/05, 64

PRIOR PAPLICATION NUMBER: 60/05, 69

PRIOR PILING DARE: 1997-08-29

PRIOR PILING DARE: 1997-08-29

PRIOR PELING DARE: 1997-08-29
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Gaps
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Best Local Similarity 50.0%; Pred. No. 25;
Matches 8; Conservative 4; Mismatches 4; Indels
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TITLE OF INVENTION: 70 Human Secreted Proteins FILE REFERENCE: PSOOIPI 2001P1

FILE REFERENCE: PSOOIPI 3001P1

CURRENT FILING DATE: 1998-03-06

EARLIER PILING DATE: 1998-03-06

EARLIER FILING DATE: 1998-03-06

EARLIER FILING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07

EARLIER PELING DATE: 1997-03-07

EARLIER PILING DATE: 1997-03-07
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R PILING DATE: 1997-05-23
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,600
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,597
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R APPLICATION NUMBER: 60/047,502
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,503
R APPLICATION NUMBER: 60/047,503
R FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,617
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
APPLICATION WINBER: 60/047,503
HILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
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APPLICATION NUMBER: 60/047,581
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-148-545-246
; Sequence 246, Application US/09148545
; Ebblication No. US20030027132A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                  | | : | |||:|:| : | 223 TWQQALTGLLERMQTY 238
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                                                                                                                                                                                                                                                                  2 TWMKTLQGLLDRIQAF 17
; SEQ ID NO 246
; LENGTH: 339
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BARLIER FILING DATE: 1997-05-23

BARLIER APPLICATION NUMBER: 60/047,596

BARLIER APPLICATION NUMBER: 60/047,612

BARLIER APPLICATION NUMBER: 60/047,612

BARLIER APPLICATION NUMBER: 60/047,612

BARLIER APPLICATION NUMBER: 60/047,612

BARLIER APPLICATION NUMBER: 60/047,613

BARLIER APPLICATION NUMBER: 60/047,613

BARLIER FILING DATE: 1997-05-23

BARLIER FILING DATE: 1997-05-23

BARLIER FILING DATE: 1997-04-11

BARLIER FILING DATE: 1997-04-12

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER PILING DATE: 1997-08-22

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER PILING DATE: 1997-08-22

BARLIER APPLICATION NUMBER: 60/056, 893

BARLIER PILING DATE: 1997-08-22

BARLIER PILING DATE: 1997-08-22

BARLIER PI
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BARLIER APPLICATION NUMBER: 60/056,910
BARLIER PILLING DATE: 1997-08-22
BARLIER PILLING DATE: 1997-08-22
BARLIER PILLING DATE: 1997-06-23
BARLIER PILLING DATE: 1997-06-22
BARLIER PILLING DATE: 1997-06-22
BARLIER PILLING DATE: 1997-06-22
BARLIER PILLING DATE: 1997-06-22
BARLIER PILLING DATE: 1997-06-23
BARLIER APPLICATION NUMBER: 60/047,594
BARLIER PILLING DATE: 1997-06-23
BARLIER APPLICATION NUMBER: 60/043,576
BARLIER PILLING DATE: 1997-06-23
BARLIER APPLICATION NUMBER: 60/065,695
BARLIER APPLICATION NUMBER: 60/065,695
BARLIER PILLING DATE: 1997-06-22
BARLIER APPLICATION NUMBER: 60/065,695
BARLIER APPLICATION NUMBER: 60/065,695
BARLIER PILLING DATE: 1997-06-22
BARLIER PILLING DATE: 1997-06-23
BARLIER PILLING DATE:

Query Match
Best Local Similarity 50.0%; Pred. No. 25;
Matches 8; Conservative 4; Mismatches 4; Indels

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Gaps

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APPLICANT: Xu, H. TILLE OF INVENTION: Identification of Essential Genes in Microorganisms
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NUMBER OF SEQ ID NOS: 78614
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LORDITICATION OF BSSENCIA
OURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR PELING DATE: 2000-03-21
PRIOR PELING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-05
PRIOR PILING DATE: 2000-09-09
PRIOR PELING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-20
PRIOR PELING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-22
PRIOR PELING DATE: 2000-10-22
PRIOR PELING DATE: 2000-11-22
PRIOR PELING DATE: 2000-12-22
PRIOR PELING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-19
PRIOR PILING DATE: 2001-02-19
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                                                                 US-112-82-122A-123B-1
US-112-82-122A-123B-1
Publication No. US20040029129A1
GENERAL INFORMATION
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Oblsen, Kari
APPLICANT: Wall, Daniel
APPLICANT: Cark, Obhn
APPLICANT: Cark, Obhn
APPLICANT: Cark, Obhn
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 TW-----MKTLOGLLDRIQAFPSSP 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTSUKT, TETSUJI
WAKAMATSU, AI
SATO, HIROYUKI
ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUGIYAMA, TOMOYASU
OTSUKI, TETSUJI
                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 10; Conserva
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APPLICANT: ISOGAL, TA
APPLICANT: SUGIYAMA,
APPLICANT: OTSUKI, TAPLICANT: WAKAMATSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-10-282-122A-42581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: MISC FEATURE

1. LOCATION: (276)

2. OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids

US-10-264-237-2238
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Sequence 1037, Application US/10408765A

Publication No. US20040101874A1

SEBERAL INFORMATION:

APPLICANT: Chosh, Soumitra S.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Taylor, Steven W.

APPLICANT: Marnock, Dale B.

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT APPLICATION NUMBER: US/10/408,765A

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1037

LENGTH: AREA
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GENERAL INFORMATION:
TITLE OF INVENTION:
TITLE OF INVENTION:
CURRENT APPLICATION NUMBER: US/10/264,237
CURRENT FILING DATE: 2002-10.04
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR APPLICATION NUMBER: PCT/US01/16450
PRIOR APPLICATION NUMBER: DCS-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-18
PRIOR FILING DATE: 2000-05-19
SOFTWARE: PLENG DATE: 2000-05-18
SOFTWARE: PLENG DATE: 2000-05-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

42.4%; Score 50; DB 15; Length 486;
Best Local Similarity 50.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismarches
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                                                       223 TWQQALTGLLERMÓTY 238
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2 TWMKTLQGLLDRIQAF 17
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
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APPLICANT: Xu, H.

APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPRENCE: ELITRA.034 US/10/282,122A
FILE REPRENCE: ELITRA.034 US/10/282,122A
CURRENT APPLICATION NUMBER: 05/191,078
FRIOR APPLICATION NUMBER: 06/191,078
FRIOR APPLICATION NUMBER: 06/203-21
FRIOR APPLICATION NUMBER: 06/203-23
FRIOR APPLICATION NUMBER: 06/203-23
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-26
FRIOR PLING DATE: 2000-05-06
FRIOR APPLICATION NUMBER: 06/230,335
FRIOR APPLICATION NUMBER: 06/230,347
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-10-23
FRIOR PLING DATE: 2000-11-27
FRIOR PLING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 66/255,931
FRIOR PLING DATE: 2001-12-27
FRIOR APPLICATION NUMBER: 66/256,636
FRIOR APPLICATION NUMBER: 66/256,636
FRIOR PLING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-09
FRIOR FILING DATE: 2001-02-06
FRIOR FILING DATE: 2001-
Sequence 45536, Application US/10282122A
Publication No. US20040029129A1
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NAME/KEY: MISC_FEATURE
LOCATION: (1897...(183)
OTHER INFORMATION: X=any amino acid
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1 LOCATION: (185)...(185)
2 OTHER INFORMATION: X=any amino acid
US-10-282-122A-45536
                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haeelbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Ohlsen, Kari
APPLICANT: Tyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Gart Grant
APPLICANT: Famingon, Robert
APPLICANT: Famingon, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Bacillus anthracis
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US-10-437-963-115384

i Sequence 115384, Application US/10437963

j Eublication No. US20040123343A1

i GENERAL INFORMATION:
    APPLICANT: La Rosa, Thomas J.
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Cao, Yongwei
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Boukharov, Andrey A.
    APPLICANT: Li, Ping
    TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
    TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
    TILE REREBENCE: 38-21(53221)B
    CURRENT APPLICATION NUMBER: US/10/437,963
    CURRENT PILING DATE: 2003-05-14
    NUMBER OF SEQ ID NOS: 204966
    SEQ ID NO 115384
    LENGTH: 213
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40.7%; Score 48; DB 14; Length 139;
Best Local Similarity 56.2%; Pred. No. 20;
Matches 9; Conservative 1; Mismatches 6; Indels
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Query Match

40.7%; Score 48; DB 16; Length 213;
Best Local Similarity 61.5%; Pred. No. 31;
Matches 8; Conservative 3; Mismatches 2; Indels
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US-10-437-963-115384
       APPLICANT: OTSUTA, KAORU
APPLICANT: NAGAI, KEIICHI
APPLICANT: TRIE, RYOTARO
APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SCHIKAMA, TSUTOMU
APPLICANT: OSSHIKAMA, TSUTOMU
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: OTSUKA, MOTOVIKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: OSSHIKAMA, TSUTOMU
APPLICANT: NASUHO, YASUHIKO
FILE REFERENCE: 084335/0160
CURRENT FILING DATE: 2002-03-12
PRIOR PLILNG DATE: 2002-03-12
PRIOR FILING DATE: 2002-01-24
PRIOR FILING DATE: 2001-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
NUMBER OF SEQ ID NOS: 3381
SOFTWARE: PATCHING DATE: 2010-09-14
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15 MQGLLDHVDAFPA 27
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ORGANISM: Oryza sativa
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US-10-282-122A-45536
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Query Match
40.7%; Score 48; DB 15; Length 299;
Best Local Similarity 42.1%; Pred. No. 45;
Matches 8; Conservative 5; Mismatches 6; Indels
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                                                                                                                                        88 ISTTKGLIIQLQALPCKPH 106
                                                                                                         4 MKTLOGLLDRIQAFPSSPH 22
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NESOUNT 15

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APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Plug
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE OF INVENTION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 17410
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Best Local Similarity 66.7%; Pred. No. 78;
Matches 10; Conservative 0; Mismatches 5; Indels
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40.7%; Score 48; DB 16; Length 500;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 10; Conservative 0; Mismatches 5; Indels
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US-10-437-963-174132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_72100C.1.pep
US-10-437-963-174130
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LOCATION: (1)..(500)
LOCATION: (1)..(500)
PEATURE INFORMATION: unsure at all Xaa locations
PEATURE:
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ORGANISM: Oryza sativa
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ORGANISM: Oryza sativa
FEATURE:
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Search completed: November 11, 2004, 07:41:45 Job time : 53.1601 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

using sw model - protein search, OM protein November 10, 2004, 14:52:32; Search time 7.51601 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-68 118 1 ATWMXTLQGLLDRIQAFPSSPH 22

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: Dirl:*
2: Dir2:*
3: Dir3:*
4: Dir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description	probable deacetyla	hypothetical prote	probable deacetyla	histone deacetylas	pyrimidine synthes	glycogen(starch) s	probable sodium-tr	fructuronate reduc	peptidyl-dipeptida	hypothetical prote	DNA-binding protei	peptidyl-dipeptida	a)	citrate synthase-l	citrate synthase -	heat shock transcr	sulfite reductase	peptidyl-dipeptida	gene APXL protein	utrophin - human	٠Ä	chitinase (EC 3.2.	hypothetical prote		窗	hypothetical prote	-dipe	MYB like protein -	peptidyl-dipeptida
SUMMARIES	ID		H65070	(A)	IO.	$\sim$	S61504		H86828	A35655	AD2572	T47523	A34171	B83605	T49157	853007	S25481	AB3636	JC2038	137183	528381	AB0589	JC7536	$^{\circ}$	64	S	F96791	805238	T48510	A31759
	DB	ı		7																										
	Length	403	403	403	296	2225	603	503	544	732	1097	1298	1312	344	480	516	527	733	1313	1616	3433	246	269	306	345	515	614	732	952	1306
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	Result No.		(7	m	4	ß	9	7	œ	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

probable tenascin dihydroorotate oxi citrate synthase-1 GP120 V3 LOOP prot conserved hypothet phosphoglycerate m phosphoglycerate m phosphoglycerate m phosphoglycerate m prophetical prote probable tyrs prot probable tyrs prot hypothetical prote conserved hypothet hypothetical prote hypothetical prote hypothetical prote	peptide synthetase rev protein - simi
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## ALIGNMENTS

RESULT 1

	A91097
	probable deacetylase [imported] - Escherichia coli (strain 0157:H7, substrain RIMD 0509
_	C;Species: Escherichia coli
	C;Date: 18-Jul-2001 #sequence revision 18-Jul-2001 #text_change 09-Jul-2004
	C;Accession: A91097
	R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.C
	gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
	DNA Res. 8, 11-22, 2001
	A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and gen
	A; Reference number: A99629; MUID:21156231; PMID:11258796
	A; Accession: A91097
	A;Status: preliminary
	A; Molecule type: DNA
	A; Residues: 1-403 <hay></hay>
	A; Cross-references: UNIPROT: Q46805; GB: BA000007; PIDN: BAB37168.1; PID: 913363217; GSPDB:
	A;Experimental source: strain O157:H7, substrain RIMD 0509952
	C;Genetics:
_	A;Gene: ECs3745
_	C;Superfamily: succinyl-diaminopimelate desuccinylase
	O Mash 13 9. Coors 61. DB 3. Tength 403.
	Query Match Total Total Similarity 50 09. Dred No 3.
	Description of Conservative 4: Mismatches 5: Indels 0: Gabs 0:

٠. م Matches

ð g hypothetical protein b2872 - Escherichia coli (strain K-12)
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Species: Bscherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Gocession: H65070
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
R;Blattner, P.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Residues: 1-403 < BLAH7
A;Residues: 1-403 < BLAH7
A;Residues: 1-403 < BLAH7
A;Residues: 1-403 < BLAH7
A;Cross-references: UNIPROT:Q46805; GB:AEG000370; GB:U00096; NID:g2367170; PIDN:AAC75910
A;Reperimental source: strain K-12, substrain MG1655
C;Superfamily: succinyl-diaminopimelate desuccinylase

ó Gaps . 0 Query Match
Best Local Similarity 50.0%; Pred. No. 3.1;
Matches 9; Conservative 4; Mismatches 5; Indels

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A;Cross-references: UNIPROT:P08955; GB:M60078; NID:g191338; PIDN:AAA63617.1; PID:g19133 R;Simmer, J.P.; Kelly, R.E.; Rinker Jr., A.G.; Scully, J.L.; Evans, D.R. J. Biol. Chem. 265, 10395-10402, 1990 A;Title: Mammalian carbamyl phosphate synthetase (CPS). CDNA sequence and evolution of A;Reference number: A35432; MUID:90285162; PMID:1972379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:J05503; NID:g191332; PIDN:AAA37062.1; PID:g191333
R;Williams, N.K.; Simpson, R.J.; Moritz, R.L.; Peide, Y.; Crofts, L.; Minasian, E.; Lea:
Gene 94, 283-288, 1990
A;Title: Location of the dihydroorotase domain within trifunctional hamster dihydroorot:
A;Reference number: PS0159; WUID:91078651; PMID:1979549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cross-references: GB:M1124; NID:g191330; PIDN:AAA37061.1; PID:g387067; Maley, J.A.; Davidson, J.N. iochem. Biophys. Res. Commun. 154, 1047-1053, 1988; Title: Identification of the junction between the glutamine amidotransferase and carb; Reference number: A30794; MUID:88309082; PMID:2900634
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A; Introns: 28/1
A; Introns: 28/1
C; Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; B
C; Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; B
C; Keywords: hydrolase; ligase; methyltransferase; multifunctional enzyme; phosphoproteil
C; Keywords: hydrolase; ligase; methyltransferase (ammonia) homology cCPA.
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F;4-1542/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain homology
F;78-354/Domain: trgd homology <TRG3
F;38-1439/Domain: trgd homology <TRG3
F;385-1439/Domain: carbamoyl-phosphate synthase (glutamine-hydrolyzing) large chain hom
F;385-1438/Domain: biotin carboxylase homology <BC1>
F;345-1801/Domain: biotin carboxylase homology <BC2>
F;4457-1801/Domain: Bacillus dihydroorotase homology <DHO>
F;1924-2222/Domain: aspartate/ornithine carbamoyltransferase homology <ACT>
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, Residues: 24-64 < MAL>
, Residues: 24-64 < MAL>
, Sciences: GB: M31927
, Simmer, J.P.; Kelly, R.E.; Rinker Jr., A.G.; Zimmermann, B.H.; Scully, J.L.; Kim, H.;
, Simmer, J.P.; Kelly, R.E.; Rinker Jr., A.G.; Zimmermann, B.H.; Scully, J.L.; Kim, H.;
, Frice. Natl. Acad. Sci. U.S.A. B7, 174-178, 1980
, Trille: Mammalian dihydroorctase: nucleotide sequence, peptide sequences, and evolution, Reference number: A34803; MUID:90115834; PMID:1967494
R;Bein, K.; Simmer, J.P.; Evans, D.R.
J. Biol. Chem. 266, 3791-3799, 1991
A;Title: Molecular cloning of a cDNA encoding the amino end of the mammalian multifunct
A;Reference number: A38653; MUID:91139675; PMID:1671675
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PMID:1982061
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A, Residues: 1403-2110 «WIL»
A, Cross-references: GB:M33702; NID:g191172; PIDN:AA37009.1; PID:g191173
A, Cross-references: GB:M3702; Maley, J.A.; Niswander, L.A.; Davidson, J.N.
Mol. Cell: Biol. 5, 1735-1742, 1985
A) Title: Construction of a cDNA to the hamster CAD gene and its application
A, Reference number: A23443; MUID:85267690; PMID:2862577
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;Residues: 2074-2225 <SHI>
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A;Residues: 156-1455 <SIM>
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A; Residues: 1-169 <BEI>
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Residues: 1-73 <RES>
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C;Genetics:
A;Gene: CC2072
C;Superfamily: accordants
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C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Accession: G87505
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Reference number: A87249; MuID:21173698; PMID:11259647
A;Accession: G87505
A;Accession: G87505
A;Residues: 1-2506 - CAULOBACTER CAUL
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carbamoyl-phosphate synthase C;Specias: Mesocricetus auratus (golden hamster) C;Date: 29-Aug-1987 #sequence revision 02-Jun-1994 #text change 09-Jul-2004 C;Accession: A38653; A35432; PS0159; A23443; A30794; A34803; I48154
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41.5%; Score 49; DB 2; Length 296;
Best Local Similarity 43.8%; Pred. No. 4.6;
Matches 7; Conservative 4; Mismatches 5; Indels
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peptidyl-dipeptidase A (EC 3.4.15.1), testis - mouse
NyAlternate names: peptidyl-dipeptidase I, testis
NyAlternate names: peptidyl-dipeptidase I, testis
C,Species: Nus musculus (house mouse)
C,Species: Nus musculus (house mouse)
C,Bate: 10-Sep-1999 #sequence_travision 10-Sep-1999 #text_change 09-Jul-2004
C,Accession: A3565
MOI Cell. Biol. 10, 4294-4302, 1990
A,Fitle: Transcription of testicular angiotensin-converting enzyme (ACE) is initiated w
A,Reference number: A35655, MUID:90318396; PMID:2164636
A,Accession: A35655
A,Accession: A35655
A,Accession: A35655
A,Accession: A35655
A,Accession: A35655
A,Accession: A35655
A,Accession: Definimary
A,Molecule type: mRNA
A,Residues: 1-73 c-HOM-A
A,Residues: 1-73 c-HOM-A
A,Cross-references: UNIPROT:P22867; GB:M55333; NID:g191589; PIDN:AAA37149.1; PID:g19159
C,Superfamily: mammalian peptidyl-dipeptidase A
C,Keywords: alternative splicing; peptidyldipeptide hydrolase; transmembrane protein; z
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AD2572
hypothetical protein all9003 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120e
hypothetical protein all9003 [imported] - Nostoc sp. (strain PCC 7120) plasmid pCC7120e
c;Species: Nostoc sp. PCC 7120
c;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
c;Accession: AD2572
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium An
A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
                                                                                                                  fructuronate reductase (EC 1.1.1.57) [imported] - Lactococcus lactis subsp. lactis (str C,Species: Lactococcus lactis subsp. lactis
C,Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-544 <STO.
A; Residues: 1-544 <STO.
A; Residues: 1-544 <STO.
A; Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                        J.; Ehrl
                                                                                                                                                                                 C.Accession: H86828
R/Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehr Genome Res. 11, 731-753, 2001
A. Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A. Reference number: A. R6625; Wuld:21235186; PMID:11337471
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Pred. No. 28;
5; Mismatches
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C;Superfamily: mannitol 2-dehydrogenase
C;Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | : | |: | SAWCRYLIGINDELESFSPSP 465
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Best Local Similarity 38.1%;
Matches 8; Conservative
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Best Local Similarity
Matches 7; Conserv
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Figure 1. 2, 193-202, 1992

Afficiency Multh, A.; Bhattacharyya, M.; Dunn, P.; Martin, C. Plant J. 2, 193-202, 1992

Affitle: Characterization of cDNAs encoding two isoforms of granule-bound starch synthas Affitle: Characterization of CDNAs encoding two isoforms of granule-bound starch synthas Afficession: S61504; MUID:93251108; PMID:1302049

Ascession: S61504

Ascession: MRNA

Ascession: S61504

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C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn
C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycogen(starch) synthase (EC 2.4.1.11) isoform I precursor - garden pea NiAlternate names: glycogen(starch) synthase C;Species: Pisum sativum (garden pea) C;Becies: 20-Jul.1996 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004 C;Accession: S51504; S72372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                          Length 2225;
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                                                                                 Score 48; DB 1;
Pred. No. 62;
5; Mismatches 6
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Pred. No. 21;
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F;252/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 WMKA--GILESDQVFTVSPH 318
                                                                                                                                                                                                                                                                                                                       3 WMKTLQGLLDRIQAFPSSPH 22
                                                                                                                                                                                                                                                                  4 MKTLQGLLDRIQAFPSSPH 22
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Best Local Similarity 50.0%;
Matches 10; Conservative
                                                                                 Query Match
Best Local Similarity 42.1%;
Matches 8; Conservative
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A;Accession: A61477
A;Status: preliminary
A;Status: preliminary
A;Molecule type: protein
A;Rosidues: 35-5; Access
A;Experimental source: kidney
C;Superfamily: mammalian peptidyl-dipeptidase A
C;Superfamily: mammalian peptidyl-dipeptidase A
F;H-34/Domain: signal sequence #status predicted <SIG>F;1-34/Domain: signal sequence #status predicted <SIG>F;35-1312/Product: peptidyl dipeptidase I #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: B33602
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bi
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-344 <STO>
A;Cross-references: UNIPROT:Q916H0, GB:AE004470; GB:AE004091; NID:g9946164; PIDN:AAG0377
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable acetylpolyamine aminohydrolase PA0321 [imported] - Pseudomonas aeruginosa (stri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Map position: 3
A;Introns: 79/3; 140/1; 168/3; 203/3; 224/3; 261/2; 301/2; 351/2; 391/3; 424/2; 461/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    oftrate synthase-like protein - Arabidopsis thaliana
N.Alternate names: protein - Arabidopsis thaliana
N.Alternate names: protein T20N10.90
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: A. Accession: T49157
R.D.A.Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, Submitted to the Protein Sequence Database, April 2000
A.Reference number: Z25017
A.Accession: T49157
A.Accession: T49157
A.Molecule type: DNA
A.Residues: I-480 -ANA
A.Residues: I-480 -ANA
A.Residues: UNIPROT:Q9LX87; EMBL:AL353022; GSPDB:GN00061; ATSP:T20N10.90
A.Experimental source: cultivar Columbia; BAC clone T20N10
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                                                                                                                                                                                                                                                                                                                                              Length 1312;
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Pred. No. 35;
                                                                                                                                                                                                                                                                                                                                              DB 1;
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Pred. No. 24;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                              39.0%; Score 46; DB 35.0%; Pred. No. 73; Live 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :| : | : | : | 889 WAQTWSNIYDLVAPFPSAPN 908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 WMKTLOGLLDRIOAFPSSPH 22
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256 ATWSQALQAAIRQIQAY 272
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ilarity 47.1%;
Conservative
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C;Superfamily: citrate synthase
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 35.0
Matches 7; Conservative
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Best Local Similarity
Matches 8, Conserva
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Best Local Similarity
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A,Gene: PA0321
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Aga171

paptidy-dipeptidase A (EC 3.4.15.1) precursor - mouse
NyAlternate names: ACE, angiotensin-converting enzyme; carboxycathepsin; dipeptidy] cart
C;Decise: Name musculus (house mouse)
C;Dete: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A34171; A29220; A61477

R;Bernstein, K.E.; Martin, B.M.; Edwards, A.S.; Bernstein, B.A.
J;Bernstein, E.B.; Martin, B.M.; Edwards, A.S.; Bernstein, B.A.
J;Reference number: A34171; MUID:8930899; PMID:2545691
A;Title: Mouse angiotensin-converting enzyme is a protein composed of two homologous dom
A;Reference number: A34171
A;Residues: 1-1312 cBER
A;Residues: 1-33 cBE2
A;Reference number: A29220; MUID:88298730; PMID:2841312
A;Residues: 1-33 cBE2
A;Residues: 1-34 cBE2
A;Residues: 1-35 cBE2
A;Residues: 1-37 cBE2
A;Residues: 1-38 cBE2
A;Residues: 1-38 cBE2
A;Residues: 1-38 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding protein-like - Arabidopsis thaliana
NyAlternate names: protein F1612.40
NyAlternate names: protein F1612.40
Sybecies: Arabidopsis thaliana (mouse-ear cress)
C;Dete: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47523
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Rudd, S.; submitted to the Protein Sequence Database, March 2000
A;Reference number: Z24468
A;Accession: T47523
A;Accession: T47523
A;Residues: 1-1298 -JOR>
A;Residues: 1-1298 -JOR>
A;Residues: 1-1298 -JOR>
A;Residues: 1-1298 -JOR>
A;Accession: A;Apposition: 3
A;Nap position: 3
A;Nate: F1612.40
       A;Molecule type: DNA
A;Residues: 1-1097 «XUR>
A;Residues: 1-1097 «XUR>
A;Ecroses: UNIPROT:Q8YJW0; GB:AP003605; PIDN:BAB77489.1; PID:g17134934; GSPDB:6A;Ecroserimental source: strain PCC 7120
C;Genetics:
A;Gene: al19003
A;Genome: plasmid
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                                                                                                                                                                                                                                                                                                                                              5; Mismatches
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                                                                                                                                                                                                                                                                                 Score 46;
Pred. No. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                      2 TWMKTLQGLLDRIQA-----FPSSP 21
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42.9%;
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Best Local Similarity 42.9
Matches 9; Conservative
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Best Local Similarity 38.5
Matches 10; Conservative
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Gaps

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citrate synthase - cucurbit
C;Species: Oucurbita sp. (cucurbit)
C;Species: Oucurbita sp. (cucurbit)
C;Accession: 553007
B;Kato, A.; Hayashi, M.; Mori, H.; Nishimura, M.
B;Kato, A.; Hayashi, M.; Mori, Sp. 1995
A;Title: Molecular characterization of a glyoxysomal citrate synthase that is synthesize
A;Reference number: S53007; MUD:95195164; PMID:7888626
A;Accession: S53007
A;Accession: S53007
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: MSNA
A;Molecule type: MSNA
A;Residues: 1-516 cKAT>
A;Cross-references: GB:D38132; NID:9975632; PIDN:BAA07328.1; PID:9975633
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Pred. No. 38;
1; Mismatches 5; Indels
     Indels
  3; Mismatches
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                                             8 QGLLDRIQAFPSSPH 22
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165 QGVLDMIQSMPNDVH 179
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173 QGLVDIIQAMPHDAH 187
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Best Local Similarity 60.0%;
Matches 9; Conservative
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8; Conservative
Matches
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NCBI_TaxID=222523;
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SEQUENCE FROM N.A.
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Q73dz0 bacillus ce
Q81yws bacillus an
Aat29609 bacillus
Q7zwrs xenopus lae
Q6dfb3 xenopus lae
Q6dfb3 xenopus lae
Q6dfb3 xenopus lae
Q8003 schizcoacch
C8112 human immun
Q46805 escherichia
C8112 human immun
Q90395 photobacter
C910077 homo sapien
Q95088 homo sapien
Q95088 homo sapien
Q91x76 homo sapien
Q91x76 homo sapien
Q91x8 homo sapien
Q91x8 homo sapien
Q91x18 homo sapien
Q91x11 rattus no
Q91x11 homan immun
Q837d2 enterococcu
                                                                                                                                                                                November 10, 2004, 14:50:40; Search time 36.8754 Seconds (without alignments) 343.270 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1825181 segs, 575374646 residues
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Q83DZ0
Q813DZ0
Q813DZ0
AAX129609
AAT29609
Q7ZW5
Q6DFB1
Q6DFB1
Q6LQN1
CAG20395
Q9LQN7
Q9CX30
Q
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                              US-10-092-750-68
118
1 ATWMKTLQGLLDRIQAFPSSPH 22
                                                                                                                                  - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Q837D2
Q9A6M1
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1: uniprot_sprot:*
2: uniprot_trembl:*
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seq length: 200000000
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Match Length DB
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No.
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	Q6euf8 oryza sativ	P27708 homo sapien	P08955 mesocricetu	Aah65510 homo sapi	Q90bm2 human immun				Q9vqx3 drosophila		Q43092 pisum sativ	Q80225 human immur	Q6c7k0 yarrowia	53
Q9ASL1	QEEUF8	PYR1 HUMAN	PYR1 MESAU	AAH65510	Q90BM2	Q7SUP8	695060	090571	Q9VQX3	Q84UE8	SSG1 PEA	080225	Q6C7K0	ALIGNMENTS
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40.7	40.7	40.7	40.7	40.7	40.3	40.3	39.8	39.8	39.8	39.8	39.8	39.8	39.8	
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The	RN [1]  RN SEGUENCE FROM N.A.  RC STRAIN=PERST, Anopples Genome Sequencing Consortium; Anopples Genome Sequencing Consortium; Anopples Genome Sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.  CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is preliminary data.  EMBL; AAAB01008900; BAA09500.2;  CREAT. AAAB01008900; BAA09500.2;  CREAT. AAAB01008900; BAA09500.2;  CREAT. AAAB01008900; BAA09500.2;  CREAT. AAAB01008800; BAA09500.2;  CREAT. AAAB01008900; BAA09500.2;  CREAT. AAA09500.2;  CAUTION. TER 593 AA, 65943 MW, 620395C348C48F6E CRC64;	Query Match       46.6%; Score 55; DB 2; Length 593;         Best Local Similarity 52.9%; Pred. No. 9.5;         Matches 9; Conservative 5; Mismatches 3; Indels 0; Gaps         Qy 1 ATWMKTLQGLLDRIQAF 17         Db 437 STWIKTLEGIIMSIQTF 453	RESULT 2 Q73DZ0 ID Q73DZ0 O73DZ0 D Q73DZ0 D Q73DZ0 D Q73DZ0 D Q73DZ0 D G73DZ0 O73DZ0 D G73DZ0 D G73DZ0 O5-UL-2004 (TrEMBLrel. 27, Created) DT 05-ULL-2004 (TrEMBLrel. 27, Last sequence update) DT 05-ULL-2004 (TrEMBLrel. 27, Last annotation update) DF Cell division inhibitor-like protein. GN CreatedLousNames=BCE0570, OS Bacteria; Firmitutes; Bacillales; Bacillus.
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Gaps

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4; Indels

Length 301;

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Cell division.
SEQUENCE 301 AA; 33595 MW; 4D2255DB55A224A3 CRC64;
                                                                                     Query Match

84.9%; Score 53; DB 2;
Best Local Similarity 42.1%; Pred. No. 9.9;
Matches 8; Conservative 7; Mismatches 4
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TIGRFAMS; TIGR01777; yfcH; 1.
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Best Local Similarity 42.1%;
Matches 8; Conservative
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AAS39505
ID AAS39505
AAS37

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AAT29609
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XX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;

XA REAG T.D., Peterson S.N., Tourasse N.J., Bailia L.M., Paulsen I.T.,

Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,

Holtzapple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,

ANDIONAY J.F., Madpu R.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,

DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,

Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,

Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Neidman W.C.,

A Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,

A Slabberg S.L., Thomason B., Friedlander A.M., Koehler T.M.,

Hanna P.C., Kolstoe A.-B., Fraser C.M.;

The genome sequence of Bacillus anthracis Ames and comparison to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Ames / isolate 0581;
Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K., Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R., Richardson P., Rubin B., Tice H.;
Submitted (JAN.2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AE017025; AAP24537.1; ---
EMBL; AE017234; AAT52817.1; ---
EMBL; AB017255; AAF52817.1; ---
TIGR; BA0515.--
PubMed=14960714;
Rasko D.A., Ravel J., Oekstad O.A., Helgason B., Cer R.Z., Jiang L., Shores K.A., Fouts D.B., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
Nelson W.C., Kolstoe A.-B., Fraser C.M., Read T.D.;
"The genome sequence of Bacilius cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pxOl.";
Nucleic Acids Res. 32:9779-988 (2004).
TIGRS, BCE0570;
TIGRS, BCE0570;
TIGRSPAMS; TIGRO1777; yfcH7.
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42.1%; Pred. No. 9.9;
ive 7; Mismatches 4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bacillus anthracis comparative genomics.";
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                        slete proteome.
33584 MW; 3E24F59EC43DFECB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cell division inhibitor-like protein.
OrderedLocusNames=BA0515, BAS0486; ORFNames=GBAA0515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                              4 MKTLOGLLDRIQAFPSSPH 22
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 42.1
Matches 8; Conservative
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                                                                                                                                                                                                                                                                           Cell division; Complete
SEQUENCE 301 AA; 3358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 423:81-86(2003).
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EMBL, AE017334; AAT29609.1; ANDEFERENCES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fasko D.A., Ravel J., Oekstad O.A., Helgason E., Cer R.Z., Jiang L., Shores K.A., Fouts D.E., Tourasse N.J., Angiuoli S.V., Kolonay J.F., Nelson W.C., Kolstce A.-B., Fraser C.M., Read T.D., "The genome sequence of Bacillus cereus ATCC 10987 reveals metabolic adaptations and a large plasmid related to Bacillus anthracis pX01."; Nucleic Acids Res. 32:977-988(2004).
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42.1%; Pred. No. 9.9;
ive 7; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacillus anthracis str. Ames 0581,
Bacteria, Firmicutes; Bacillales; Bacillus;
Bacillus cereus group; Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                                                                                              BCE0570.
Bacillus cereus (strain ATCC 10987).
Bacteria, Firmicutes; Bacillales; Bacillaceae, Bacillus.
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                                                                                                                                                                                                                                                                     02-MAR-2004 (TrEMBLrel. 27, Created)
04-MAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
Cell division inhibitor-like protein.
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01-JUN-2004 (TrEMBLrel. 27, Last sequence update)
01-JUN-2004 (TrEMBLrel. 27, Last annotation update)
cell division inhibitor-like protein.
                                                                                                                                                                                                                 301 AA.
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                                                                                                                                                                                                                 PRT;
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                                                          88 IQTTKGLIKQLÖALÞAKPH 106
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4 MKTLQGLLDRIQAFPSSPH 22
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Length 301;

DB 2;

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SEQUENCE FROM N.A.
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                                               Q6DFB3
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RESULT 7

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Rlausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A blatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Bigleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
Willalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Pahey J., Helton E., Retteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevohenko Y., Bouffard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.B.,
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                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                   MGC53840 protein.
Xenopus laevis (African clawed frog).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUB-Embryo;
Klein S., Strausberg R.;
Submitted (FBB-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC0467742; AAH46742.1; -.
InterPro; IPR008380; Purine_nucl.
Pfam; PF05761; 5 nucleotid; nucleotid; 864A8C88A2FA4004 CRC64;
SEQUENCE 486 AĀ; 56809 MW; 864A8C88A2FA4004 CRC64;
                                                                                                                                                                                                                                                                 01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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Pred. No. 9.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Embryo;
MEDLINE=22388257; PubMed=12477932;
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TISSUE=Embryo;
MEDLINE=22341132; PubMed=12454917;
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88 IQTTKGLIKQLQALPAKPH 106
                                                                  4 MKTLOGLLDRIQAFPSSPH 22
  ilarity 42.1%; Pr
Conservative 7;
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365 TWLQALTGLLERMONF 380
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                                                                                                                                                                                                                        PRELIMINARY;
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8355;
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Matches
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TISSUE=Cocytes,

X MEDINE=2388257; PubMed=12477932;

X Alausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Aluschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Aluschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

BA Diarchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Brask S.A., MorEwan P.J., McKernan K.J., Malek J.A., Mullahy S.J.,

R. Broak S.A., MorEwan P.J., McKernan K.J., Lu X., Gibbs R.A.,

R. Richards S., Worley K.C., Hale S. Garcia A.M., Gay L.J., Hulyk S.W.,

R. Pinky J., Helton E., Ketteman M., Madan A., Golfies S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

R. Rodriguez A.C., Grimmood J., Schmutz J., Myers R.M., Butterfield Y.S.,

R. Aones S.J., Marra M.A.;

R. Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                     01-OCT-2004 (TrEMBLrel. 28, Created)
01-OCT-2004 (TrEMBLrel. 28, Last sequence update)
10-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Hypothetical protein.
Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein.
SEQUENCE 583 AA, 66687 MW, 758688FF98B0B558 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TIMI_SCHPO STANDARD; PRT; 817 AA. 036033; Q9P379; Treated)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Hypothetical protein C19B12.01 in chromosome 19RPAnames=SPAC19B12.01, SPAC4F10.21;
583 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22341132; PubMed=12454917;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        462 TWLQALTGLLERMQNF 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 TWMKTLQGLLDRIQAF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Oocytes;
Klein S., Strausberg R.;
Submitted (JUL-2004) to the
EMBL; BC076827; AAH76827.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                Xenopodinae; Xenopus
NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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Fri Nov 12 14:55:57 2004

201 AA.

PRT;

PRELIMINARY;

OBALI2

RESULT 9 U

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RX STRAIN=2718 (ARAIN=2718)

RX MEDLINE=21844(1); PubMed=11859360; DOI=10.1038/nature724;

RA MOGO V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., RA Bagnam D., Bowaman S., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M., RA Gorlins M., Connor R., Cronin A., Davis P., Fidialgo J., Hodgson G., Rapiros S., Goble A., Hamin N., Harris D., Hidalgo J., Hodgson G., RA Holroyd S., Hornsby T., Howarth S., Hunckle E.J., Hunt S., Jagels K., Amoney P., Moules L., Jones M., Leather S., McDonald S., McLean J., RA Mooney P., Moule S., Miggall K., Murche E.J., Hunt S., Jagels K., Amoney P., Moule S., Miggall K., Murche E.J., Hunt S., Jagels K., Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S., Stevens K., Sharp S., Stevens K., Sharp S., Stevens K., Sharp S., Stevens K., Statior R., Taylor R., Tivey A., Walsh S.V., Warren T., Whichead S., Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B., Modeljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S., R. Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M., R. Begre P., Caddeu B., Dreano S., Gloux S., Lelaure V., Mottier S., Lucas M., Carlado L., Jimenez S., Hunt C., Moore K., Hurst S.M., Abaga R.R., Cruzado L., Jimenez J., Sanchez M., Galzon A., Garzon A., Thod A. Baga R.R., Cruzado L., Jimenez J., Sanchez M., Galzon A., Grutti L., Lowe T., Moreno S., Armetrong J., Potashkin J., R. Shpakovski G.V., Ussery D., Barrell B.G., Nurse P., R. The Genome sequence of Schizosaccharomyces pombe.",

R. Matter 415: 811-880(2002).

C. -- SIMILARITY: CONTAINS 4 TPR FEPERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the BMBL outstation the buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Pred. No. 39;
6; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8B05FA55E06E6E21 CRC64;
                        Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam, PF00515; TPR, 2.
PROSITE, PS50005; TPR, 3.
PROSITE, PS50293; TPR REGION; 1.
Hypothetical protein; Repeat; TPR repeat.
Schizosaccharomyces pombe (Fission yeast)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPR 1.
TPR 2.
TPR 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, 298980, CAB11723.1; -.
EMBL, AL390814; CAC00549.1; -.
GeneDB Spombe, SPAC19812.01; -.
InterPro; IPR001440; TPR.
InterPro; IPR008941; TPR-like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.18;
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Best Local Similarity 47.1
Matches 8; Conservative
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658
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555 5
625 6
817 AA;
                                                                 Schizosaccharomyces.
                                                                                                                            SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=4896
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SEQUENCE
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MEDIJNE=22440026; PubMed=12551997;
MEDIJNE=22440026; PubMed=12551997;
Gordon M., De Oliveira T., Bishop K., Coovadia H.M., Madurai L.,
Engelbrecht S., van Rensburg B.J., Mosam A., Smith A., Cassol S.;
"Molecular characteristics of human immunodeficiency virus type 1
subtype C viruees from Kwazulu-Natal, South Africa: implications for vaccine and antiretroviral control strategies.";
J. Virol. 77:2587-2599(2003).
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STRAIN=KI2 / MG1655;
STRAIN=W426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Coat protein; Envelope protein; Glycoprotein; Transmembrane.
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Enterobacteriaceae; Escherichia.
NCBI_TaxID=562, 217992, 83334;
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STRAIN-66.HI, CFT073 / ATCC 700928 / UPEC;
MEDILINE-22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
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Tarim M., De Oliveira T., Bishop K., Coovadia H.M., Madurai S.

Tarim M., De Oliveira T., Bishop K., Coovadia H.M., Madurai S.

Bugelbrecht S., van Rensburg E.J., Mosam A., Smith A., Cassol Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.

EMBL, AV137054; AAN16003.1; -

GO, GO:0019028; Caviral capsid; IEA.

GO, GO:00019018; F:structural molecule activity; IEA.

FinterPro. IPRO00716; GP120: 1.
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01-NOV-1997 (Rel. 35, Last sequence update)
05-UDL-2004 (Rel. 44, Last annotation update)
Hypothetical protein yegy.
Name-ygeX; OrderedLocusNames=b2872, C3450, Z4211, EC83745;
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                                  01-WAR-2003 (TrEMBLrel. 23, Created)
01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                     Viruses, Retroid viruses, Retroviridae, Lentivirus.
NCSI_TaxID=11676,
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                                                                                                                                                                          Envelope glycoprotein (Fragment).
                                                                                                                                                                                                                                                                      Human immunodeficiency virus 1.
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Best Local Similarity 47.1%;
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Escherichia coli 06, and
Escherichia coli 0157:H7.
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NON TER
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SO DE REPRESENTANTA DE PERCENTANTA D
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"Genome analysis of Photobacterium profundum reveals the complexity of
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Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F.,
Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vezzi A., Campanaro S., D'Angelo M., Simonato F., Vitulo N., Lauro F., Cestaro A., Malacrida G., Simionati B., Cannata N., Bartlett D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome Analysis of Photobacterium profundum reveals the complexity of
Putative deacetylase.
OrderediocusNames=PBPRA1992;
Photobacterium profundo (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Photobacterium profundum (Photobacterium sp. (strain SS9)).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Photobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                  high pressure adaptations.";
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
BMBLJ, CR378669; CAG20395.1;
InterPro; IPR001261; ArgE dapE.
InterPro; IPR001261; ArgE dapE.
InterPro; IPR002933; Peptidase_M20.
Pfam; PF01546; Peptidase_M20;
PROSITE; PS00158; ARGE DAPE CPG2 1; UNKNOWN_1.
PROSITE; PS00148; ARGE DAPE CPG2 1; UNKNOWN_1.
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Cestaro A.;
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; CR378669; CAG20395.1; -.
SEQUENCE 405 AA; 45299 MW; 53BB7A9CD45DA868 CRC64;
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Submitted (MAR-2004) to the BMBL/GenBank/DDBJ databases
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10-WAY-2004 (TrEMBLrel. 27, Last sequence update)
10-WAY-2004 (TrEMBLrel. 27, Last annotation update)
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Best Local Similarity 50.0%; Pred. No. 27;
Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 51; DB 2; Pred. No. 27; 4; Mismatches
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SEQUENCE FROM N.A.
STRAIN=889;
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SEQUENCE FROM N.A.
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SEQUENCE 405 AA
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                                                                                                                                                                                                                                                                                                                                                  Valle G.;
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CAG2035
ID CAG20
AC CAG20
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DT 10-MA
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RA STRAIN-0157:H7 / RIND 0509952 / EHEC;

MEDLINE-21156231; PubMed=11258796;

MEDLINE-21156231; PubMed=11258796;

MA HAYASHI T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA HAYASHI T., Makino K., Makayama K., Marata T., Tanaka M., Tobe T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T., Tanaka M., Tobe T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T., Tanaka M., Tobe T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T., Tanaka M., Tobe T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T., Tanaka M., Tobe T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T.,

RA HAT C.-G., Ohtsubo E., Nakayama K., Marata T.,

RA HAT C.-G., Ohtsubo E., Nakayama K.,

RA HAT C.-G., Ohtsubo E.,

RA HAT C.-G.,

RA HAT C.-G.

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R REMEL; AE016/65; AAN81895.1; -.

R REMEL; AP016/65; AAN81895.1; -.

R REMEL; AP016/65; AAN81895.1; -.

R REMEL; AP016/65; AAN81895.1; -.

R PIR; A91097; A91097.

R PIR; B85942; E85942.

R PIR; B85942; E85842.

R ECOGENE; E82867; -.

R ECOGENE; E12867; -.

R ECOGENE; E13055; YgeY.

R ECOGENE; E13055; YgeY.

R ECOGENE; E13055; YgeY.

R ECOGENE; PEPLIGASE M20.

R INTERPRO; IPR00293; PepLIGASE M20.

R Ffam; PF015/64; PepLiGASE M20.

R Ffam; PF015/64; PepLiGASE M20.

R PROSITE;

R COMPLETE A93 AA; 44804 MW; 87937D1224403886 CRC64;
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D., Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T., Mobley H.L.T., Donnerberg M.S., Blattner F.R.; "Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli."; Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).
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                                                                                                                                                                                                                                          STRAINSO157:H7 / EDL933 / ATCC 700927 / EHEC;
BEDLINE-21074935. PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Bosfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
"Genome sequence of entrer F.R.;
"Genome sequence of entrer hand."
Nature 409:529-533(2001).
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OGLONI;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43.2%; Score 51; DB 1; 50.0%; Pred. No. 27;
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Gaps

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Length 405;

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Gaps

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Indels

Length 405;

Matches

ð g RESULT 11 D6LQN1 Mus musculus (Mouse).

RESULT 13

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RA Pulabeda-14/102039;
RA Wakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Wakamateu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishili S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Murakahi M., Kanda K., Yokoi T., Furuya T., Kikkawa B., Omura Y.,
RA Takahashi M., Kanda K., Yokoi T., Yamashita H., Murakawa M., Yamazaki M.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Masashino K., Yuuki H., Oshima A., Saaski N., Aotsuka S.,
Aoshikawa Y., Matanabe T., Sugiyama A., Takemoto M., Kawkami B.,
RA Maraaki M., Watanabe T., Sugiyama A., Takemoto M., Kawkami B.,
RA Yamazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawkami B.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
RA Amazaki M., Watanabe T., Sugiyama A., Takemoto M., Kawkami B.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
Rujimori Y., Komiyama M., Tashiro H., Tanigami A., Pulwara T.,
Rujimori Y., Watanabe T., Moguchi S., Itoh T., Shigeta K., Sana A.,
Rujimori Y., Watanabe T., Moguchi S., Itoh T., Shigeta K., Sana A.,
Rushumina S., Ruji Y., Ozaki K., Hara H., Itoha Y., Watanaba M., Kawabai M., Kawabai M., Katanaba M., Kawabai M., Kawabai M., Kawabai M., Kawabai M., Kawabai M., Sasaki M.,
Rujimori Y., Watanabe T., Nomura N., Kawabai Y., Watanaba M., Kawabai Y., Wamashita R., Nakai K., Yada T., Nomura N., Ohara O., Isogai T., Sugano S.,
Rujimori Y., Ompula J., Ohara O., Isogai T., Sugano S.,
Rujimori Y., Watanaba M., Matanat
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 15, Last annotation update)
01-Mar-2004 (TrEMBLrel. 26, Last annotation update)
Mus musculus 13 days embrry liver cDNA, RIKEN full-length enriched
library, clone:2510015F01 product:CDNA FLJ13933 FIS, CLONE
Y79AAA1000795, WERKLY SIMILAR TO CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC
3:1.3.5) homolog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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EMBL, AKO02128; BAA92095.1; -.

Interpro; IPRO0380; Purine_nucl.

Pfam; PF05761; 5 nucleocid; 1.

SEQUENCE 120 AA, 14303 MW; C9605BF684726B2C CRC64;
                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein FLJ11266.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 153 AA.
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                     PRELIMINARY;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                               TISSUE=Placenta;
PubMed=14702039;
                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
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                                                   09NUM7;
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                     Q9NUM7
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1D 026733
AC 09C73
DT 01-JU
DT 01-JU
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DE 3.3-34AA
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REGUENCE FROM N.A.

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REGUENCE FROM N.A.

RA Adachi J., Alzawa K., Akahira S., Pukuda S., Fukunishi Y., Puruno M., Arawa T., Baran A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F., RA Imotani K., Ishi Y., Itoh M., Izawa M., Kasukwa T., Kato H., RA Imotani K., Ishi Y., Konno H., Kouda M., Koya T., Kuto H., RA Kawai J., Kojima Y., Konno H., Nishi K., Nomura K., Numazaki R., Ohno M., RA Mateuyama T., Miyazaki A., Nishi K., Nomura K., Sakai C., Sakai K., RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K., RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T., RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshino M., RA William M., Hayashizaki Y., Submitted (UUL-2000) to the EMBL/GenBank/DDBJ databases.

B. MGD; MGI:1972211 S.10015F01Rik.

DR MGD; MGI:1972211 S.10015F01Rik.

DR MGD; MITCHPLO; IPRO08380; Purine _nucl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         The FANTOM Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazati Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

MEDIATE 2772HL/67; TISSUE=Liver;

Shibate K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shibate K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,

Shonto H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,

Sumi N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,

Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,

Yujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,

Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,

Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

"RIKEN integraced sequence analysis (RISA) system-384-format

Genome Res. 10:1757-1771(2000)
                Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                               RIKEN FANTOM COnsortium; "Punctional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42.4%; Score 50; DB 2; Length 153; 50.0%; Pred. No. 15; tive 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF05761; 5 nucleotid; 1.
SEQUENCE 153 AA; 18301 MW; D5397211877B00E7 CRC64;
                                                                                                                       STRAIN=CS7BL/6J; TISSUE=Liver;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.;
"High-efficiency full-length cDNA cloning.";
                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Liver;
                                                                                                                                                                                                                 Meth. Enzymol. 303:19-44(1999)
                Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                               NCBI_TaxID=10090;
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Gaps

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Query Match Best Local Similarity Matches 8; Conserva

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O95888;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein.
Hypothetical protein.
Eukaryota, Metazoa; Conordata, Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96207227; PubMed=8619474;
Andersson B., Wentland M.A., Ricafrente J.Y., Liu W., Gibbs R.A.,
"A 'double adaptor' method for improved shotgun library
construction."
Anal. Biochem. 236:107-113(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97264341; PubMed=9110174; MEDLINE=97264341; PubMed=9110174; Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing."; Genome Res. 7:353-358(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 42.4%; Score 50; DB 2; Length 390; Best Local Similarity 50.0%; Pred. No. 38; Matches 8; Conservative 4; Mismatches 4; Indels
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Mei G., Yu W., Gibbs R.A.;
Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
EMBL, AF1317181, AAD20044.1; -.
InterPro; IPR008380; Purine_nucl.
Fyfam; PF05761; 5_nucleotid; 1.
Hypothetical profes
                                                                                                                   390 AA
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32 TWQQALTGLLERMQTY 47
2 TWMKTLOGLLDRIGAF 17
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Search completed: November 10, 2004, 15:53:30 Job time: 38.9524 secs

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RESULT 1
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Sequence 5, Appli
Sequence 9, Appli
Sequence 1875, A
Sequence 1875, A
Sequence 6403, Ap
Sequence 7565, Ap
Sequence 26885, A
Sequence 15, Appl
Sequence 15, Appl
Sequence 15, Appl
Sequence 1875, A
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                                                         November 10, 2004, 14:55:47; Search time 13.879 Seconds (without alignments) 143.349 Million cell updates/sec
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2. /cgn2 6/prodata1/liaa/5B_COMB.pep:*

3. /cgn2 6/prodata1/liaa/6A_COMB.pep:*

4. /cgn2 6/prodata1/liaa/6B_COMB.pep:*

5. /cgn2 6/prodata1/liaa/PCTUS COMB.pep:*

5. /cgn2 6/prodata1/liaa/PCTUS COMB.pep:*

6. /cgn2 6/prodata1/liaa/PCTUS COMB.pep:*
          GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-924-620C-5
US-08-924-620C-5
US-08-924-620C-5
US-09-248-796A-18735
US-09-248-796A-18735
US-09-253-6403
US-09-252-991A-24609
US-09-252-991A-24609
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US-09-252-991A-26995
US-09-252-991A-26995
US-09-107-532A-4745
US-09-107-532A-4745
US-09-107-532A-4745
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US-09-107-532A-4745
US-09-107-65-991A-26997
US-09-107-65-991A-26997
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US-08-352-071-56
US-08-352-071-67
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                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                          478139 seqs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
                                                                                                                                        Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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161
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Sequence 63, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 335, App
Sequence 34348, A
Sequence 23262, A
Sequence 23306, A
Sequence 27538, A
Sequence 27638, A
Sequence 27638, A
Sequence 27638, A
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTAME: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/159,340A

FILING DATE: 24-NOV-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 37,642

REFERENCE/DOCKET NUMBER: 37,642

REFERENCE/DOCKET NUMBER: 37,642

TELECOMMUNICATION INFORMATION:

TELEFRAX: (512) 474-7577

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHRACTERISTICS:

LENGTH: 926 amino acids

LENGTH: 926 amino acids
US-08-461-004A-63
US-08-36-014A-67
US-08-36-014A-57
US-09-198-452A-33
US-09-270-767-34348
US-09-270-767-34348
US-09-248-796A-24444
US-09-248-796A-24444
US-09-248-796A-24368
US-09-248-796A-24368
US-09-258-991A-23306
US-09-258-991A-23306
US-08-898-976-4
US-08-898-976-4
US-08-898-976-4
US-08-898-976-4
US-09-252-991A-27686
US-09-252-991A-27686
US-09-252-991A-27686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/06159340A
| Patent No. 5565352 |
| Patent No. 5565352 |
| GENERAL INFORMATION: |
| APPLICANT: Hochstrasser, Mark |
| TITLE OF INVENTION: DEUBIQUITINATING ENZYME: CO. |
| TITLE OF INVENTION: AND METHODS |
| NUMBER OF SEQUENCES: 44 |
| CORRESSED NUMBERS Abrold, White & Durkee |
| STREET: P.O. Box 4433 |
| CITTLE: Houston |
| STATE: Texas |
| COUNTRY: USA |
| COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
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65;
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31.1%; Score 50; DB
Best Local Similarity 34.5%; Pred. No. 65;
Matches 10; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ANRKOPKPNNSSTAYYNFTGVSILPSYKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 926 amino acids
TYPE: amino acid
STRANDEDNESS: single
   TOPOLOGY: linear
MOLECULE TYPE: protein
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APPLICANT: Johnston, Robert E.
APPLICANT: Davis, Nancy L.
APPLICANT: Simpson, Dennis A.
TITLE OF INVENTION: System for the In Vivo Delivery and
TITLE OF INVENTION: Systemsion of Heterologous Genes in the Bone Marrow
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                 3; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 29.5%; Score 47.5; DB 3; Length 2512; Best Local Similarity 42.3%; Pred. No. 5.3e+02; Matches 11; Conservative 6; Mismatches 6; Indels 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER REARABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEB: Bell Seltzer Park & Gibson, P.A. STREET: 1211 East Morehead Street
CITY: Charlotte
STRIE: No. 6008035th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1782 AARKEPTPPASNSSESLHLSFGGVSM 1807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ANRKOPKP---NNSSTAYYNFTGVSI 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/801,263
FILING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/09102248
Patent No. 6008035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAWE: Sibley, Kenneth D.
REGISTATION UNDER: 31,665
REFERENCE/DOCKET NUMBER: 5470-
TELECOMMUNICATION INFORMATION:
TELEFONS: 919-820-2200
TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 9:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2512 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 2512 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-102-248-9
                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                       US-08-801-263A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 4
US-09-102-248-9
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US-09-367-764-9
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APPLICANT: Franz, Charles M.A.P.
APPLICANT: Franz, Charles M.A.P.
TITLE OF INVENTION: NO. 6403082elBacteriocins, Transport and Vector System and Method
FILE REPRENCE: 660.000508
CURRENT APPLICATION NUMBER: US/08/924,629C
CURRENT APPLICATION NUMBER: US 60/026,257
PRIOR PILING DATE: 1996-09-05
NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3.1
SBQ ID NO 5
LENTH: 717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jacobuston 19, Application US/08801263A

| Sequence 9, Application US/08801263A
| Patent No. 5811407
| GENERAL INFORMATION:
| APPLICANT: Johnston, Robert E. APPLICANT: Johnston, Dennis A. TITLE OF INVENTION: System for the In Vivo Delivery and TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow NUMBER OF SEQUENCES: 12
| CORRESPONDENCES: 12
| ADDRESSEE: Bell Seltzer Park & Gibson, P.A. STREET: 1211 East Morehead Street
| CITY: Charlotte | COUNTRY: USA | COUNTRY: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 29.8%; Score 48; DB 4; Length 717; Best Local Similarity 44.4%; Pred. No. 95; Mismatches 12; Conservative 5; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATCHIN PC COMPATIBLE
COMPUTER: APENIN PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: PATENTIN BATCH:
APPLICATION NUMBER: US/08/801,263A
FILLING DATE: 19-FEB-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   120 NKMTKAHFNEEWTGVSIFIAPNPTYKP 146
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                                                                                                   Sequence 5, Application US/08924629C
Patent No. 6403082
GENERAL INPORMATION:
APPLICANT: Stiles, Michael E.
APPLICANT: Vederas, John C.
APPLICANT: Wan Belkum, Maxius J.
APPLICANT: Worobo, Randy W.
APPLICANT: Worobo, Randy W.
APPLICANT: Morobo, Rodney J.
APPLICANT: Morobo, Rodney J.
APPLICANT: Greer, G. Gordon
APPLICANT: Leisner, Jorgen J.
APPLICANT: Leisner, Jorgen J.
APPLICANT: Leisner, Jorgen J.
APPLICANT: Pron, Alsion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5470-TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-420-2200
TELEPHONE: 919-481-3175
                                          RESULT 2
US-08-924-629C-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-924-629C-5
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and David Bush
AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                US-09-538-092-503
) Sequence 503, Application US/09538092
) Sequence 503, Application US/09538092
) Patent No. 6753314
) GENERAL INFORMATION:
) APPLICANT: Giot, Loic
) APPLICANT: Mansfield, Traci A.
) TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same FILE REPERNENCE: 1596-542
) CURRENT APPLICATION NUMBER: US/09/538,092
) CURRENT FILING DATE: 2000-03-29
) PRIOR PILING DATE: 1999-04-01
) PRIOR APPLICATION NUMBER: 60/127,352
) RIOR FILING DATE: 2000-02-01
) NUMBER OF ERQ ID NOS: 1387
) SOFTWARE: CuraPat/SeqFormatter Version 0.9
) SEQ ID NO 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 632;
                                    29.2%; Score 47; DB 4; Length 501; 50.0%; Pred. No. 86; ive 4; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESCEE: GENOME THERAPEUTICS CORPORATION STREET: 100 Beaver Street
CITY: Mailtham
CITY: Mailtham
CITY: Mailtham
STATE: Massachusetts
COUNTY: USA
ZIP: 0.2354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Unn-1998
FRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FRIENG DATE: 14 May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
28.9%; Score 46.5; DB 4;
Best Local Similarity 34.5%; Pred. No. 1.4e+02;
Matches 10; Conservative 7; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 NRKOPKPNNSSTAYYNFTGVS-ILPSYKP 30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
ENTEROCOCCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6403, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Saccharomyces cerevisiae
                                                                                                                                                                                                                                             474 NNNNSSYYNVTNHSQSPS 491
                                                                                                                                                                                            10 NNSSTAYYNFTGVSILPS 27
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                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
                                        Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-107-532A-6403
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Sequence 18735, Application US/09248796A

Sequence 18735, Application US/09248796A

Sequence 18735, Application US/09248796A

Sequence 18735, Application US/09248796A

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

APPLICANT: Roith Weinstock et al

APPLICANT: Roith Weinstock et al

TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: 107196-132

FRIOR APPLICATION NUMBER: US 60/074,725

FRIOR FILING DATE: 1998-02-13

FRIOR APPLICATION NUMBER: US 60/074,725

FRIOR FILING DATE: 1998-08-13

FRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 18735

LENGTH: 501
                                                                                                          APPLICANT: Johnston, Robert E.
APPLICANT: Johnston, Robert E.
APPLICANT: Davis, Nancy L.
APPLICANT: Simpson, Dennis A.
TITLE OF INVENTION: System for the In Vivo Delivery and
TITLE OF INVENTION: Expression of Heterologous Genes in the Bone Marrow
NUMBER OF SEQUENCES:
ADDRESSES:
ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 29.5%; Score 47.5; DB 4; Length 2512; Best Local Similarity 42.3%; Pred. No. 5.3e+02; Matches 11; Conservative 6; Mismatches 6; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                            AUDKESSEE: BELL SELECTE FAIR & GLEBOH, F.A.
GLIY: Charlotte
STATE: 1211 East Morehead Street
STATE: 0.00 6583121th Carolina
COUNTRY: UGA
ZIP: 28234
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN RC-DOS/MS-DOS
SOFTWARE: PATENTIN NUMBER: US/09/367,764
APPLICATION NUMBER: US/09/367,764
ATING DATE: 19-FEB-1997
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 31,665
RELEPAN: 919-881-3175
THELEPAN: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1782 AARKEPTPPASNSSESLHLSFGGVSM 1807
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Sequence 9, Application US/09367764
Patent No. 6583121
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 919-881-3175
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-18735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Gaps

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US-09-248-796A-26885

Sequence 26885, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: VOLIBIC ACID AND THERAPEUTICS

TITLE OF INVENTION: VOMBER: US/09/248,796A

TITLE OF INVENTION: WOMBER: US/09/248,796A

CURRENT RILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 26885

LENGTH: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ch 28.3%; Score 45.5; DB 4; Length 60; il Similarity 45.5%; Pred. No. 10; 10; Conservative 5; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Redmond, Mark J.
APPLICANT: Redmond, Mark J.
APPLICANT: Ijaz, Mohammed K.
APPLICANT: Jaz, Mohammed K.
APPLICANT: Jaz, Mohammed K.
APPLICANT: Jaz, Mohammed K.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTISON & POERSTER
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                                                                                                                                                                                             Query Match 28.6%; Score 46; DB 4; Length 308; Best Local Similarity 42.9%; Pred. No. 67; Matches 9; Conservative 5; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7565
LENGTH: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 20, Application US/07603133B ; Sequence 20, Application US/07603133B ; Patent No. 5298244 ; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 ANR-VAKSGNSTFSYFNFSAIS 49
                                                                                                                                                                                                                                                                                                                                                                                                   203 PKPNFSTTIQALFTKLGLVPA 223
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                                                                                                                                                                                                                                                                                                                                                                7 PKPNNSSTAYYNFTGVSILPS 27
                                                                                                                                                                    ORGANISM: Acinetobacter baumannii
US-09-328-352-7565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-248-796A-26885
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ZIP: 940
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Sequence 24609, Application US/09252991A

Sequence 24609, Application US/09252991A

Sequence 24609, Application US/09252991A

Sequence 24609, Application US/09252991A

Sequence 24609

Sequence 24609

Sequence 24609

Sequence 24609

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 24609

LENGTH: 84
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Patent No. 656258

GENERAL INC. 656258

GENERAL TO. 656258

GENERAL TO. 656258

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNI FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTC99-03PA
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28 6%; Score 46; DB 4; Length 84;
Best Local Similarity 37:5%; Pred. No. 13;
Matches 9; Conservative 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.9%; Score 46.5; DB 4; Best Local Similarity 40.9%; Pred. No. 1.5e+02; Matches 9; Conservative 7; Mismatches 5;
                          ATORNEY/AGENT INFORMATION:
NAME: ATINELLO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELEFANDE: (781)893-5007
TELEFANDE: (781)893-5007
INFORMATION FOR SEQ ID NO: 6403:
SEQUENCE CRARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...682
SEQUENCE DESCRIPTION: SEQ ID NO: 6403:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Enterococcus faecium
           APPLICATION NUMBER: 60/051571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7 PKPNNSSTAYYNFTGVSILPSYKP 30
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                                                                                                                                                                                                                                                                                                              LENGTH: 682 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-252-991A-24609
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US-09-328-352-7565
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28.3%; Score 45.5; DB 3; Length 776; 45.8%; Pred. No. 2.5e+02; tive 3; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: «Unknown>
SOFFWARE: ASCII
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Denek
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 40,489
REGISTRATION NUMBER: 60/051571
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...67
;
SEQUENCE DESCRIPTION: SEQ ID NO: 4745:
US-09-107-532A-4745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                                                                                                                                   454 KPNNSQ-EYYEIAGRFSLISLVPS 476
                                                                                        8 KPNNSSTAYYNFTG----VSILPS 27
                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUT
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 67 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
Query Match 28.3°
Best Local Similarity 45.8°
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR
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Pred. No. 2.5e+02;
3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIF: Z0006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BLM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,397A
FILING DATE: 07-JUL-1993
ATCASSIFICATION NUMBER: 30,988
REGISTRATION NUMBER: 30,988
REGISTRATION NUMBER: 29311-20003.03
TELEFROE (202) 887-1500
TELEFROE: (202) 887-1500
TELEFRA: (202) 887-1503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15. Application US/08089397A
Patent No. 6086880
GENERAL INFORMATION:
APPLICANT: FRENHICK, PATRICK J.
APPLICANT: FRENHICK, PATRICK J.
APPLICANT: FRENHICK, ANDREW A.
APPLICANT: IJAZ, MOHAMMAD K.
APPLICANT: GILCHRIST, JAMES B.
APPLICANT: REDMOND, MARK J.
TITLE OF INVENTION: ROTAVIRUS VACCINES
                                                                                                                                        9313-0004.00
    APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        454 KPNNSQ-EYYEIAGRFSLISLVPS 476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 2000 Pennsylvania Avenue, CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8 KPNNSSTAYYNFTG----VSILPS 27
                                                                ATTORNEY/AGENT INFORMATION:
NAME: RODINS, RODERTS 1.
REGISTRATION NUMBER: 33.208
REFERENCE/DOCKET NUMBER: 9313
TELECOMMUICATION INFORMATION:
TELECHONE: (415) 327-255
                                                                                                                                                                                               TELEFAX: ...
TELEX: 706141
INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 776 amino acids: TYPE: AMINO ACID
TYPE: AMINO ACID
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                    28.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        : 776 amino acids amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
28.3
Best Local Similarity 45.8
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                            , MOLECULE TYPE: protein US-07-603-133B-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 2.
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                          FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-089-397A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D
COUNTRY:
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GENERAL INFORNATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDCMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT PAPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 26937

LENGTH: 114

TYPE: PRI

CREATION PRIOR PRIOR OF SEQ ID NOS: 33142

SEQ ID NO 26937

LENGTH: 114

TYPE: PRI

CREATION PRIOR PRIOR OF SEQ ID NOS: 33142

SEQ ID NO 26937

LENGTH: 114

TYPE: PRI

CREATION PRIOR PRIOR OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
28.0%; Score 45; DB 4; Length 114;
Best Local Similarity 42.1%; Pred. No. 28;
Matches 8; Conservative 3; Mismatches 8; Indels
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Search completed: November 10, 2004, 15:57:21 Job time : 13.879 secs

96 RKNPKPNKNLSNISRFAGI 114

4 RKOPKPNNSSTAYYNFTGV 22

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Gaps ; 0 1623, Ap 253829,

Sequence

Sequence 5010, Ap Sequence 50110, Ap Sequence 5011, Ap Sequence 272561, A Sequence 180243, Sequence 56187, A Sequence 56187, A Sequence 160, App Sequence 10926, Sequence 25, Appl Sequence 281, Appl Sequence 281

Perfect score: Sequence: Scoring table:

Title:

Searched:

OM protein

on:

Run

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5 US-10-369-493-1623

5 US-10-369-493-1623

5 US-10-424-599-253829

5 US-10-425-114-49900

5 US-10-425-114-49457

6 US-10-425-114-49457

6 US-10-425-114-49457

6 US-10-425-114-599-247789

6 US-10-427-599-247789

6 US-10-427-599-247789

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6 US-10-437-598-8

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6 US-10-188-495-13

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6 US-10-188-495-13

6 US-10-188-495-11

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6 US-10-188-495-11

6 US-10-188-495-11

6 US-10-188-495-11
                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
Sequence 69, Appl
Sequence 15135, A
Sequence 12135, A
Sequence 231460,
Sequence 231699,
Sequence 192571,
Sequence 190072,
Sequence 123010,
Sequence 2545, Ap
Sequence 230249,
Sequence 217690,
Sequence 230249,
                                                                           November 11, 2004, 02:43:24; Search time 72.4911 Seconds (without allgnments) 146.426 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                   Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/NGG_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOF_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USOF_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/NGOF_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/NGOF_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/USIOB_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/USIOD_PUBCOMB.pep:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-739-930-5692
US-10-16-76-12135
US-10-424-599-231460
US-10-424-599-23569
US-10-424-599-192717
US-10-424-599-192717
US-10-425-115-190072
US-10-425-115-230249
US-10-425-115-230249
US-10-425-115-230249
US-10-425-115-230249
US-10-425-115-230249
US-10-425-115-230249
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161
1 EANRKQPKPNNSSTAYYNFTGVSILPSYKP 30
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                                                                                                                                                                                                                     1568699 segs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                          - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Match 1
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APPLICANT: KOVALIC, DAVIG K.

TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
TITLE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
TITLE OF INVENTION: 98-21 (53377) B
CURRENT APPLICATION NUMBER: US/10/739,930
CURRENT FILING DATE: 2003-12-18
NUMBER OF SEQ ID NOS: 11088
SEQ ID NO 5692
LENGTH: 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 14; Length 423;
22;
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                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: ARATH-23APR03-C122594_1.p
US-10-739-930-5692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              477 EOKPETPKPQIAVIPNNASTA----TAAALLPSHKP 508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EANRKOPK-----PNNSSTAYNFIGVSILPSYKP 30
                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(771)
FEATURE:
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 RKQPKPNNSSTAYYNFTGVSILPS----YKP 30
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34.2%; Score 55; DB
Best Local Similarity 43.8%; Pred. No. 22;
Matches 14; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-101-156-761-12135

Sequence 12135, Application US/10156761

Sequence 12135, Application US/10156761

Sequence 12135, Application US/10156761

SPELICANT: USEDA, HARDO

APPLICANT: ISEDA, HARDO

APPLICANT: ISENEAM, UNN

APPLICANT: HARDA, HRSHI

APPLICANT: HARTKAM, HROSHI

APPLICANT: HARTORI, MASAHIRA

TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES

FILE REFERENCE: 249-262

CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT APPLICATION NUMBER: JP 2001-204089

PRIOR FILING DATE: 2001-05-30

PRIOR APPLICATION NUMBER: JP 2001-272697

PRIOR FILING DATE: 2001-08-02

NUMBER OF SEQ ID NOS: 15109
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Ublication No. UG220040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptomyces avermitilis US-10-156-761-12135
                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 4
US-10-424-599-231460
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
EBNGTH: 40
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TILLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TILLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 237197
LENGTH: 455
TYPE: PRT
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(532323)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NO 231460 EDGING SEQ ID NO 231460
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US-10-424-599-283698
                                                                                                                                                                                                                                               ; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_5102C.1.pep
US-10-424-599-231460
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 33.9%; Score 54.5; DB 15; Best Local Similarity 50.0%; Pred. No. 2.8; Matches 11; Conservative 4; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.9%; Score 53; DB 15; Best Local Similarity 43.5%; Pred. No. 2.7; Matches 10; Conservative 5; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 283698, Application US/10424599 Publication No. US20040031072A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 NRKOPKPNNSSTAYYNFIGVSIL 25
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Larbazuk, Brad

Larbazuk, Brad

TITLE OF INVENTION: Block Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: 12/0/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 123010
LENGTH: 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Slater, Seven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Ghen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
ENG FILING DATE: 2002-02-1
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                                                                                            DB 17; Length 130;
15;
                                                                                                                                             11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT4530_25886C.1.pep
US-10-437-963-123010
                  ; OTHER INFORMATION: Clone ID: MRT4577_104928C.1.pep US-10-425-115-190072
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                            Score 52; DB ... Pred. No. 15; 3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                         Sequence 123010, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION: APPLICANT: La Rosa, Thomas J. APPLICANT: Zhou, Yihua APPLICANT: Cao, Yongwei; APPLICANT: Wu, Wei
                                                                                                                                                                                                                                            45 KPDPFPNOKLCAYFPFKAVDILPT 68
                                                                                                                                                                                           4 RKOPKPNNSSTAYYNFTGVSILPS 27
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Sequence 2545, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
                                                                                            Query Match
Best Local Similarity 41.7%;
Matches 10; Conservative
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  FEATURE:
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Kovalic David K
APPLICANT: Kovalic David K
APPLICANT: Town Vihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 192571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . Sequence 19072, Application US/10425115
Sequence 19072, Application US/10425115
Publication No. US20040214272A1
Publication No. US20040214272A1
Publication No. US20040214272A1
APPLICANT: La Rosa, Thomas J.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Dants
FILE REFERENCE: 38-21 (53222)
FILE REFERENCE: 38-21 (53222)
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 190072
LENGTH: 130
                                                                                                                         Length 455;
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                                              ) OTHER INFORMATION: Clone ID: PAT_MRT3847_56213C.1.pep US-10-424-599-237197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Clone ID: PAT_MRT3847_15913C.1.pep
US-10-424-599-192571
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32.3%; Score 52; DB 15; L
Best Local Similarity 43.8%; Pred. No. 7;
Matches 14; Conservative 5; Mismatches 11;
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LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
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LOCATION: (1)..(68)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                 Query Match 32.6%; Score 52.5; DB Best Local Similarity 41.9%; Pred. No. 55; Matches 13; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EANRKQPKPNNSSTAYYN--FTGVSILPSYKP 30
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                                                                                                                                                                                                                     9 PNNSST----AYYNFTGVSI---LPSYKP 30
                                                                                                                                                                                                                                               16 PNTNSTPSVYNSAPYSYTGVSSVPPIPTYEP 46
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ORGANISM: Glycine max
ORGANISM: Glycine max
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ORGANISM: Zea mays
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US-10-424-599-192571
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Query Match
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Sequence 230249, Application No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Con, Yongue
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
TITLE OF INVENTION: Plants
GURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 23049
LENGTH 268
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Squence 217690, Application Wo. US20040214272A1

GRNERAL INFORMATION:
GRNERAL INFORMATION:
GRNERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Co, Yongua
APPLICANT: Shou, Yihua
APPLICANT: Shou, Yihua
APPLICANT: So, Yongua
APPLICANT: So, Yongua
APPLICANT: Soon
APPLICANT: So
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                                                                                                                                                               Query Match 31.7%; Score 51; DB 14; Length 230; Best Local Similarity 37.0%; Pred. No. 41; Matches 10; Conservative 5; Mismatches 12; Indels
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31.7%; Score 51; DB 17; Length 268;
Best Local Similarity 58.8%; Pred. No. 49;
Matches 10; Conservative 3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: MRT4577_130130C.1.pep US-10-425-115-217690
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(268)
FEATURE INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                   106 KRKPTPPPSDGLYYVFRGKRIKKSFRP 132
                                                                                                                                                                                                                                                                                                                                             4 RKOPKPNNSSTAYYNFTGVSILPSYKP 30
; TYPE: PRT
; ORGANISM: Schizosaccharomyces pombe
US-10-369-493-2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            147 TANLHFTGVMLDPSYQP 163
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Zea mays
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US-10-425-115-230249
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Sequence 27, Application US/10362010

) Sequence 27, Application US/10362010

) Publication No. US20040038247A1

GENERAL INFORMATION:

APPLICANT: Branner, Sidney

APPLICANT: Tan, Yin, Hwee

ITILE OF INVENTION: AND PHARMACUTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR

ITILE OF INVENTION: AND PHARMACUTICAL COMPOSITIONS AND METHODS UTILIZING SAME FOR

ITILE OF INVENTION: US/10/362,010

CURRENT PAPLICATION NUMBER: US/10/362,010

CURRENT PILING DATE: 2003-08-19

NUMBER OF SEQ ID NOS: 27

SOFTWARE: PATEUTIN VERSION 3.2

SEQ ID NO 27

LENGTH: 502

LENGTH: 502

TYPE: PRT
                                                                                                                                                                                RESULT 13
US-10-425-114-59044
; Sequence 59044, Application US/10425114
; Sequence 59044, Application US/10425114
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Jingdong
; APPLICANT: Liu, Yihua
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei F
; TILE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TILE OF INVENTION: Noleic Acid Molecules and Other Molecules Associated With
; TILE OF INVENTION: Noleic Acid Molecules and Other Molecules Associated With
; TILE OF INVENTION: NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 59044

LENTH: 381
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Best Local Similarity 47.4%; Pred. No. 1.4e+02;
Matches 9; Conservative 1; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.1%; Score 50; DB 15; Length 38 Best Local Similarity 34.6%; Pred. No. 1e+02; Matches 9; Conservative 7; Mismatches 10; Indels
                            Indels
                            10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Clone ID: 700076533 FLI.pep
Best Local Similarity 34.6%; Pred. No. 97;
Matches 9; Conservative 7; Mismatches
                                                                                                              301 EADRKRPNMSNMGELFESITGGHLMP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  322 EADRKRPNMSNMGELFESITGGHLMP 347
                                                                               1 EANRKOPKPNNSSTAYYNFTGVSILP 26
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US-10-362-010-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Zea mays
FEATURE:
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us-10-092-750-69.rapb

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RESULT 15

US-10-369-493-1623

US-10-369-493-1623

Sequence 1623, Application US/10369493

Publication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
ITILE OF SEQ ID NOS: 47374

SEQ ID NO 1623
IDENOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 1623
IDENOR PLANTS WITH 1926
ITILE PROPERTIES
ITILE PROPERTIES
INVENTION: P
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November 10, 2004, 14:52:32; Search time 10.2491 Seconds (without alignments) 281:634 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                             - protein search, using sw model
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US-10-092-750-69 161 1 EANRKQPKPNNSSTAYYNFTGVSILPSYKP 30 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	hyr	probable transcrip	genome polyprotein	hypothetical prote	ruml protein - fis	Rumlp - fission ye	alpha-glucosidase	multiple sugar-bin	deubiquinating enz	hypothetical prote	hypothetical prote	seri	probable iron (III	iron(III) dicitrat	hypothetical prote		suga		tein	g G	ran	ď	e de	a]	ä	al	raJ	hypothetical prote
SUMMARIES	ΠD	969	982	B72655	562	213	44	T40233	$\sim$	AG3554	S39344	T18429	C71529	T36717	E71808	H64694	T26135	AC2865	B97642	E95990	T14580	T14816	T40873	ᇊ	S77167	215	T48615	T06119	MINWVS	F96742
	DB	!		7																										
	Length	771	158	228	3014	3262	230	230	864	218	926	1711	563	673	841	842	1829	354	354	355	391	436	963	339	401	420	468	1711	2512	225
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	Score			52		51.5	51	51	51	50.5	20	20	4.9	49	4.9	49	49		œ	œ,		•	•	48	48	48	48	48	47.5	47
	Result No.		7	٣	4	£Ω	v	7	α	σı	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

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peptidoglycan synt	hflK protein VC034	proline transporte	hypothetical prote	probable protein k	hypothetical prote	protein T12C24.12	probable purine nu	hypothetical prote	DNA (cytosine-5-)-	conserved hypothet	S-layer-like array	cyclin-dependent c	cell division prot	cell division prot	5-hydroxytryptamin
E86823	E82334	T47713	G64483	C84922	AF2320	G86259	S38042 ·	G85090	S59604	\$60083	A75526	T41101	AD1786	AF1410	I57942
C)	N	2	7	N	N	N	N	(7)	N	N	N	N	(7)	(7)	N
357	395	439	544	617	411	522	632	1512	1534	239	280	288	367	369	437
29.5	29.5	29.5	29.5	29.5	28.9	28.9	28.9	28.9	28.9	28.6	28.6	28.6	28.6	28.6	28.6
47	47	47	47	47	46.5	46.5	46.5	46.5	46.5	46	46	46	46	46	46

# ALIGNMENTS

EHH.OOOE BAAAAAAAC	RESULT 1 T49567 Phypothetical protein F7J8.250 - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress) C.Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004 C.Species: Almerman, W.; Grueneisen, A.; Wambutt, R.; Bancroft, I.; Mewes, H.W.; Le submitted to the Protein Sequence Database, January 2000 A.; Reference number: Z23018 A.; Accession: T45967 A.; Status: preliminary A.; Molecule type: DNA A.; Status: Dreliminary A.; Molecule type: DNA A.; Molecule type: DNA A.; Mesidues: 1-771 cBEV- A.; Cross-references: UNIPROT: Q9LFA9; EMBL: AL137189 A.; Experimental source: cultivar Columbia; BAC clone F7J8 A.; Map position: 5
A A	Ajīntrons: 91/3; 248/3; 319/1; 374/1; 396/2; 431/3; 462/3; 507/1; 610/3; 628/1; 672/3; A;Note: F7J8.250
	Query Match 36.6%; Score 59; DB 2; Length 771; Best Local Similarity 41.7%; Pred. No. 2.4; Matches 15; Conservative 5; Mismatches 6; Indels 10; Gaps 2;
σд	Qy 1 EANRKOPKPNNSSTAYYNFTGVSILPSYKP 30 
ждооо	RESULT 2 D89829 conserved hypothetical protein SA0559 [imported] - Staphylococcus aureus (strain N315) C;Species: Staphylococcus aureus C;Sate: 10-May-2001 #sequence revision 10-May-2001 #text change 09-Jul-2004
OKE .	C; Accession: D89829  R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogu ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89829
A;Status: preliminary
A;Residuse: preliminary
A;Residuse: 1-158 «KUR»
A;Cross-references: UNIPROT:Q95W10; GB:BA000018; PID:g13700494; PIDN:BAB41791.1; GSPDB:A;Genetics:
A;Genetics:
A;Genetics:

32.3%; Score 52; DB 2; Length 158; 47.6%; Pred. No. 3.9; Query Match Best Local Similarity ö

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UNDECLICATED ALCOLD INTEGERS OF TREEDING TO STATE OF TAXABLE OF TA
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Nature 367, 236-242, 1994
A;Title: Regulation of progression through the Gl phase of the cell cycle by the ruml(+
A;Reference number: S41043; MUID:94166876; PMID:8121488
A;Accession: S41043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:P40380; EMBL:X77730; NID:945668; PIDN:CAA54786.1; PID:9456;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule_type: DNA_ARAURA
A;Residues: 1-3262 <KURA
A;Cross-references: UNIPROT:08YTQ8; GB:BA000019; PIDN:BAB74354.1; PID:g17131748; GSPDB:
A;Experimental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rumip - fission yeast (Schizosaccharomyces pombe)
C,Species: Schizosaccharomyces pombe
C,Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C.Species: Schizosaccharomyces pombe
C.Date: 31-Mar-1992 #sequence_revision 14-Sep-1994 #text_change 09-Jul-2004
                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 ANRKOPKPN----NSSTAYYNFT------GVSILPSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 32.0%; Score 51.5; DB 2; 1
Best Local Similarity 37.5%; Pred. No. 1.5e+02;
Matches 15; Conservative 4; Mismatches 8;
pred. No. 1.2e+02;
6; Mismatches 12;
                                                                                                                                                                                                                                                                                                                                                                                                             lypothetical protein all2655 [imported] - Nostoc sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Accession: T40233
R;Moreno, S.; Wood, V.; Rajandream, M.A.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: rum1
A;Map position: 2
C;Superfamily: Schizosaccharomyces rum1 protein
                                                                                                                                                                                                      1403 ETAKKMNKPGRKAVAYYRGLDVAVIPA 1429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 KRKPTPPPSDGLYYVFRGKRIKKSFRP 132
                                                                                                                         1 EANRKOPKPNNSSTAYYNFTGVSILPS 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RKOPKPNNSSTAYYNFTGVSILPSYKP 30
ilarity 33.3%;
Conservative 6
    Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Accession: S41043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Gene: all2655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Matches
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S41043
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RyChamberlain, R.W.; Adams, N.J.; Taylor, L.A.; Simmonds, P.; Elliott, R.M.
Biochem. Biophys. Res. Commun. 236, 44-49, 1997
A/Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant A/Rcession: JC520; MuID:97366593; PMID:9223423
A/Title: The complete coding sequence of hepatitis C virus genotype 5a, the predominant A/Rccession: JC5620
A/Molecule type: mRNA
A/Rccession: JC5620
A/Molecule type: mRNA
A/Rccession: JC5620; MuID:97366593; PMID:9223423
A/Molecule type: mRNA
A/Rccession: JC5620; MuID:97366593; PMID:9223424243
A/Rccession: JC5620; MuID:97366593; PMID:922349/Product: molecule polyprotein
C/Rccession: JC5620; MuID:97366593; PMID:9729461664
A/Rccession: Major envelope protein B #status predicted < MRE>
F/192-199/Product: monstructural protein NS1 #status predicted < NS2>
F/108-1616/Product: nonstructural protein NS4 #status predicted < NS2>
F/108-1616/Product: nonstructural protein NS4 #status predicted < NS2>
F/108-1616/Product: nonstructural protein NS4 #status predicted < NS3>
F/1
                                                                                                                                                                                                                                                                                                                                                                                                genome polyprotein - hepatitis C virus (isolate EUH1480)
N;Contains: capsid protein C; envelope protein M; hepacivirin (EC 3.4.21.98) (nonstructu protein NS4a; nonstructural protein NS4b; nonstructural protein NS5 C;Species: hepatitis C virus
C;Species: hepatitis C virus
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
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        ö
                                                                                                                                                                                                                                                                                                                                                                           probable transcription activator TENA APE0669 - Aeropyrum pernix (strain K1)
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            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.3%; Score 52; DB 2; Length 228; llarity 40.0%; Pred. No. 6; Conservative 3; Mismatches 7; Indels
            8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 EVLREEPAPTNE--AYVNFMIATCSTGTALECMVSLLPCY 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
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        3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32.3%; Score 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Superfamily: transcription activator tenA
                                                                                                                                                                    122 NEEAVAYYKEQGFTILRSYQP 142
                                                                                          30
                                                                                      10 NNSSTAYYNFTGVSILPSYKP
                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
Matches 16; Conserv
                 10;
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                 Matches
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Gaps

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RESULT 10
S19344
debujidunating enzyme SSV7 - yeast (Saccharomyces cerevisiae)
N.Alternate names: debujidunating anzyme DAPA, protein D4270; protein D4270; protein C. December Saccharomyces cerevisiae D4270; protein D4270; protein C. December Saccharomyces cerevisiae D4270; protein D4270; protein C. December S40421344 feequence_revision D3494-1994 flext change 09-Jul-2004
R. Mary 1944 feequence_revision D4349-1994 flext change 09-Jul-2004
R. Mary 1945 flext 1982 flext 1982
R. Mary 1942 flext 1982 flext 1982
R. Mary 1943 flext 1982 flext 1982
R. Mary 1944 flext 1983
R. Mary 1944 flext 1984
R. Mary 1984
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A; Residues: 1-326, TX, 328-344, F', 346-374, TASW', 379-382, I', 384-406, T', 408-542, FRS'
A; Residues: 1-326, TX, 328-344, F', 346-374, TASW', 379-382, I', 384-406, T', 408-542, FRS'
A; Cross-references: EMBL: L08070; NID:g172729; PIDN: AA35105.1; PID:g172730
B; Bloecker, H.; Brandt, P.
Submitted to the Protein Sequence Database, July 1996
A; Reference number: S67587
A; Reseronce number: S67887
A; Accoule type: DNA
A; Residues: 1-926 < BLO>
                                                                                                                                                                                                                                                                       Length 218;
                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                       2;
                                                                                                                                                                                                                                                                  Query Match 31.4%; Score 50.5; DB Best Local Similarity 46.4%; Pred. No. 9.4; Matches 13; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              170 KEPEVNDTKT--YN-NGVKVVPSYLLKP 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 KOPKPNNSSTAYYNFTGVSILPSY--KP
                     strain 16M
          A, Experimental source:
C,Genetics:
A,Gene: BMEII0360
A,Map position: II
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alpha-glucosidase (EC 3.2.1.20) - Rhizomucor circinelloides f. circinelloides C; Species: Rhizomucor circinelloides f. circinelloides C; Date: 10 but 1906 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Jun-2000 C; Date: 10-Jul-1996 #sequence_revision 20-Jul-1996 #se
submitted to the EMBL Data Library, June 1998

A;Reference number: 221915

A;Accession: T40233

A;Accession: T40233

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-230 < MOR>-

A;Residues: 1-230 < MOR>-

A;Escidues: 1-230 < MOR>-

A;Cross-references: UNIPROT: P40380; EMBL: ALO23796; PIDN: CAA19370.1; GSPDB: GN00067; SPDB: A;Experimental source: strain 972h-; cosmid c32F12

C;Genetics:
A;Gene: SPDB: SPBC32F12.09

A;Map position: 2

C;Superfamily: Schizosaccharomyces rum1 protein
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Pred. No. 8.4;
5; Mismatches 12; Indels
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Best Local Similarity 37.0%;
Matches 10; Conservative 5
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Best Local Similarity 41.7%;
Matches 10; Conservative
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A; Residues: 1-841 <ARN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
                                                                                                                                                                                    C; Accession: T36717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C0345w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Species: Plasmodium falciparum
C;Sacession: T18429
R;Lawson, D.; Bowman, S.; Barrell, B.
submitted to the EMBL Data Library, August 1997
A;Reference number: Z18935
A;Accession: T18429
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1711 < LAW>
A;Residues: 1-1711 < LAW>
C;Genetics: UNIPROT:077322; EMBL:298547; NID:e1325376; PID:e1325381; PIDN:CABILI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypotherical protein CT326 - Chlamydia trachomatis (serotype D, strain UW3/Cx)
C,Species: Chlamydia trachomatis
C,Saccesion: C71529
R.Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
A;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
A;Reference number: A71570; MUD:99000809; PMID:9784136
A;Reference number: A71570; MUD:99000809; PMID:9784136
A;Accession: C71523
A;Astus: DNA
A;Residues: 1-563 -ARN>
A;Residues: 1-563 -ARN>
A;Residues: 1-563 -ARN>
A;Residues: 1-563 -ARN>
A;Residues: C,Genetics: Serotype D, strain UW-3/Cx
C;Genetics: A;Genetics: A;Genetic
A;Cross-references: EMBL:274365; NID:g1431526; PIDN:CAA98887.1; PID:g1431527; MIPS:YDR0¢
A;Experimental source: strain $288C
C;Genetics:
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Pred. No. 46;
                                                                                                                                                                                                                                                                                                                                                                    Query Match
31.1%; Score 50; DB 2; Length 926;
Best Local Similarity 34.5%; Pred. No. 59;
Matches 10; Conservative 6; Mismatches 13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 50; DB 2; Length 171
Pred. No. 1.2e+02;
1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: SGD:DOA4; SSV7; UBP4
A;Cross-references: SGD:SO002476; MIPS:YDR069c
A;Map position: 4R
C;Superfamily: deubiquinating enzyme SSV7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 ANRKOPKPNNSSTAYYNFTGVSILPSYKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      490 ANSTIPSLNNISICSGNSTIRPVLPS 515
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Best Local Similarity 57.9%;
Matches 11; Conservative 1
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ilarity 46.2%;
Conservative
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Best Local Similarity
Matches 12; Conserv
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RESULT 13 T36717

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R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKenn son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L. Matura 388, 539-547, 199.
A;Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C. A;Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A;Reference number: A64520; MUID:97394467; PMID:9252185
                                                                                                                                                      Niversell, 19.7, Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, June 1999
A; Reference number: 221612
A; Accession: T36717
A; Attains preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-673 < MUR>
A; Residues: 1-673 < MUR>
A; Cross-references: UNIPROT: Q9XA16; EMBL: AL079308; PIDN: CAB45215.1; GSPDB: GN00070; SCOEIA; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable iron (III) dicitrate transport protein - Helicobacter pylori (strain J99)
C;Species: Helicobacter pylori
A;Variety: strain J99
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
R;Alm, R.A; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, B.D.; Doig, P.C.; Smith, D.R.; Ives, C.; Gibson, R.; Merberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.; Nature 397, 176-180, 1999
A;Aitle: Genomic sequence comparison of two unrelated isolates of the human gastric pat A;Reference number: A71800; MUD:99120557; PMID:9923682
A;Accession: E71808
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C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein kinase homolog
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A;Experimental source: strain J99
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A,Status: preliminary, nucleic acid sequence not shown, translation not shown
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C.Species: Helicobacter pylori
C.Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C.Accession: H64694
probable serine/threonine protein kinase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
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C,Superfamily: Mycobacterium tuberculosis probable pknB protein;
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30.4%; Score 49; DB
Best Local Similarity 36.0%; Pred. No. 57;
Matches 9; Conservative 6; Mismatches
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A;Residues: 1-842 <TOM>
A;Cross-references: UNIPROT:025950; GB:AE000640; GB:AE000511; NID:g2314572; PIDN:AAD0844
C;Gent Codon: GTG
A;Start codon: GTG
C;Superfamily: ferrichrome-iron receptor; tonB-dependent receptor amino-terminal homolog
                                                                                                                                                                                                                         Query Match
Best Local Similarity 60.0%; Pred. No..73;
Matches 9; Conservative 1; Mismatches 5; Indels
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Search completed: November 10, 2004, 15:55:06 Job time: 11.2491 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 14:50:40; Search time 50.2847 Seconds (without alignments) 343.270 Million cell updates/sec Run on:

US-10-092-750-69 161 1 EANRKQPKPNNSSTAYYNFTGVSILPSYKP 30

Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Q91fa9 arabidopsis	_		Q6mm10 bdellovibri		Q95i61 gadus morhu					ਰ	Aas96987 desulfovi	Q86i28 dictyosteli	Q81ib1 bacillus ce	Q70h33 fowlpox vir	Q9j599 fowlpox vir	Cae52664 fowlpox v	. Q6gbm7 staphylococ					Q9yea4 aeropyrum p			Q935q3 salmonella			gadus	Q92442 mucor javan	Q8d121 synechococc
SUMMARIES	dī	Q9LFA9	Q934G7	Q82EL3	Q6MM10	CAE79696	095161	Q9Z3X7	MYC_DROME	Q89HH5	Q8TA73	Q728T7	AAS96987	Q86128	Q81IB1	Q70H33	097599	CAE52664	Q6GBM7	Q6GJ66	Q8NXU4	Q99W10	Q7A745	Q9YEA4	Q96E51	Q8L341	093503	QBYTQ8	RUM1 SCHPO	095158	AGIU_MUCJA	Q8DL21
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	Length	771	351	423	. 183	183	271	609	717	304	321	351	351	411	423	1766	1766	1766	158	158	158	158	158	228	230	206	119	3262	230	329	864	1702
d	Query Match	36.6	34.5	34.2	33.9	33.9	33.5	m	33.5	N	$\alpha$	N	N	N	$^{\circ}$	a	N	32.9	N	N	N	N	N	N	N	N	N	N	31.7	Н	31.7	31.7
	Score	59	55.5	55		4.	54	54	54	53	53	53	53	53	53	53	53	53	52	52	52	52	52	52	52	S	51.5	٠	51	51	51	51
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Q8i2p8 plasmodium Q8yd17 brucella me Q8tx36 drosophila Q8tv8 brucella su Q9vcg drosophila Q8pn90 xanthomonas O98273 gadus morhu P94168 actinobacil Q7vk57 helicobacte Q8q5j9 fugu rubrip Q6cvt9 kluyveromyc Q9aqf3 clostridium P32571 saccharomyc Q7322 plasmodium
Q812P8 Q8YD17 Q8YD17 Q8T3Z6 Q8P426 Q8P400 Q9P518 P94168 Q9VG57 Q8QC479 Q6CVT9 Q6CVT9 UBP4 YEAST
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ALIGNMENTS

nte) odate) phyta; Tracheophyta; core eudicots; rosids;	cki J., , Lemcke K.,	1; 10; Gaps
ed) ed) annotation update) annotation update) ress). phyta; Embryophyta; Tra	[1]] Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Bevan M., Zimmermann W., Grueneisen A., Wambutt R., Kalicki J., Wohldmann P., Smith A., Bancroft I., Mewes H.W., Rudd S., Lemcke Mayer K.F.X.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. [2] SEQUENCE FROM N.A. SEQUENCE FROM N.A. SUBDMITTED (JUL-2000) to the EMBL/GenBank/DDBJ databases. BU Arabidopsis sequencing project; Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases. BUARDISTISSES FROM SERVIT	Sequence update) a Sequence of indels a Sequence update) annotation update)
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PRELIMINARY; OCO (TrEMBirel. 15 OCO (TREMBirel. 15 OCO (TREMBirel. 15 CCAI protein F7J8 CAI protein F7J8 A. S. 250; A. Viridiplantae; A. V	(1) SEQUENCE FROM N.A. SEQUENCE FROM N.A. Wohldmann P., Smith A., Bancroft I., Wayer K.F.X.; Submitted (JAN-2000) to the EMBL/Geni (2) SEQUENCE FROM N.A. SEQUENCE FROM N.A. SUDMITTED (JUL-2000) to the EMBL/Geni EMBL, ALISTI89; CAB68855.1; SUDMITTED (JUL-2000) to the EMBL/Geni EMBL, ALISTI89; CAB68855.1; GO, GO:0005622; C:intracellular; IEA GO, GO:0005725; F:double-stranded RNI InterPro; IPR004174; NIF. SMART; SM0057; CPDC; 1.	Ty Match 36.6%; Scoches 15; Conservative 5; Conservative 6; Co
LEA		Query Match Best Local Sim Matches 15; QY 1 EA Db 477 EQ RESULT 2 Q934G7 AC DT 01-DEC-2001 DT 01-DEC-2001 DT 01-MAR-2004 DF 01-MAR-2004
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Fri Nov 12 14:55:58 2004

33.9%; Score 54.5; DB 2; Length 183;

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Query Match
                                                  Gaps
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Query Match 34.2%; Score 55; DB 2; Length 423; Best Local Similarity 43.8%; Pred. No. 30; Matches 14; Conservative 4; Mismatches 8; Indels
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4 RKQPKPNNSSTAYYNFTGVSILPS----YKP 30
                                                                                                                                                      Acetyltransferase
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05-JUL-2004
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                                                                                                                                Baron C., Rouot B., "Brucella suis homologue of the Agrobacterium tumefaciens chromosomal virulencia ene chve sesential for sugar utilization but not for survival in macrophages.", J. Bacteriol. 183:5343-5351(2001).

Interpro, IPR001761; PeriplaBP/Lacl.

Pfam; PF00532; Peripla BP/Lacl.
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                                                                                                                Alvarez-Martinez M.T., Machold J., Weise C., Schmidt-Eisenlohr H.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C., Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T. Kikuchi H., Shiba T., Sakaki Y., Hattori M., "Genoe T. "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptomyces avermitilis.
Bacteria, Actinobacteria, Actinobacteriaes, Streptomycineae, Streptomycetaceae, Streptomyces.
NCBI_TaxID=33903,
                                                                                                                                                                                                                                                                                                    DB 2; Length 351;
                Brucella suis.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                              sugar-binding protein.
EF566482F1F3132A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).

BMB., AP005039; BAC72313.1; -.

Complete proteome; Hypothetical protein.

SEQUENCE 423 AA; 46345 MW; CDC14CA678A3517D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRL 8165;
MEDLINE=21477403; PubMed=11572948;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 24, Last sequence update) (TrEMBLrel. 24, Last annotation update)
                                                                                                                                                                                                                                                                                                                              4.
                                                                                                                                                                                                                                                                                                                                                                                                                                               423 AA
                                                                                                                                                                                                                                                                                                  34.5%; Score 55.5; D
48.3%; Pred. No. 20;
tive 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                       302 RKEPEVNDTKT--YN-NGVKVVPSYLLKP 327
                                                                                                                                                                                                                                                                                                                                                     4 RKOPKPNNSSTAYYNFTGVSILPSY--KP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=MA-4680;
MEDLINE=22608306; PubMed=12692562;
                                                                                                        MEDLINE=21405735; PubMed=11514518;
                                                                                                                                                                                                                                                  1 21
22 351 81
351 AA; 38077 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
OrderedLocusNames=SAV4601;
                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 48.3'
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                              SEQUENCE FROM N.A.
                                                        NCBI_TaxID=29461;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-2003
01-JUN-2003
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                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q82EL3
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
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Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.; "A predator unmasked: life cycle of Edellovibrio bacteriovorus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rendulic S., Jagtap P., Rosinus A., Eppinger M., Baar C., Lanz C., Keller H., Lambert C., Evans K.J., Goesmann A., Meyer F., Sockett R.E., Schuster S.C.;
"A predator unmasked: life cycle of Bdellovibrio bacteriovorus from a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales; Bdellovibrionaceae; Bdellovibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bdellovibrio bacteriovorus.
Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales;
Bdellovibrionaceae; Bdellovibrio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acyltransferase, Complete, protecme, Transferase.
SEQUENCE 183 AA, 20648 NW, 9742371BF55E0973 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           183 AA; 20648 MW; 9742371BF55E0973 CRC64;
                                                                                                                                                                     (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
(TrEMBLrel. 27, Last annotation update)
ferase (EC 2.3.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=HD100 / DSM 50701 / ATCC 15356 / NCIB 9529;
PubMed=14752164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genomic perspective.";
Science 303:689-6202(2004).
BMB., BX842651; CAB79696.1;
GO, GO:0008415; F:acyltransferase activity; IEA.
GO, GO:016740; F:transferase activity; IEA.
InterPro; IER000182; GCM5acetyl trans.
PF00583; Acetyltransf_1; T
102 RKVAKANNASMTYF-LSGVYLLPEEKRDLYKP 132
                                                                                                                             183 AA.
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33.9%; Score 54.5; D
Best Local Similarity 52.2%; Pred. No. 14;
Matches 12; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    135 PNNSSIRYLTKYGFTSVATHPNY 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2004 (TrEMBLrel. 27, Created) 02-MAR-2004 (TrEMBLrel. 27, Last seq 02-WAR-2004 (TrEMBLrel. 27, Last ann Acetyltransferase (EC 2.3.1.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 PNNSSTAY---YNFIGVSILPSY 28
                                                                                                                                  PRT;
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Science 303:689-692(2004).
EMBL; BX842651; CAE79696.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acyltransferase; Transferase.
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                                                                                                                                                                                                                                                               OrderedLocusNames=Bd1838;
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Gaps

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Length 609;

RESULT 6

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MEDLINE=20156006; PubMed=10731132; DOI=10.1126/science.287.5461.2165;

X MEDLINE=20156006; PubMed=10731132; DOI=10.1126/science.287.5461.2165;

A Adams M.D. Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

Sutron G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen D.X.,

A Arrin G., Wortman J.R., Yandell M.D., Andrews P.Fannkoch C., Baldwin D.,

A Arril J.F., Agbayani A., An H.-J., Andrews P.Fannkoch C.R., Miklos G.L.G.,

A Arril J.F., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.M., Basu A., Berman B.P., Bhandari D., Bolshakov S.,

A Brixton G.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,

RA Gebry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila Myc is oncogenic in mammalian cells and plays a role in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-Oregon-R, William B. S. W., Cheng P.F., Parkhurst S.M., Eisenman R.N.; Mallant P., Shilo Y., Cheng P.F., Parkhurst S.M., Eisenman R.N.; Myc and Max homologs in Drosophila."; Science 274:1523-1527 (1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallant P., Shiio Y., Cheng P.F., Parkhurst S.M., Eisenman R.N., submitted (CCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., FUNCTION, SUBUNIT, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W4S7; O96903; P91665; O5-JUL-2004 (Rel. 44, Created) O5-JUL-2004 (Rel. 44, Last sequence update) O5-JUL-2004 (Rel. 44, Last annotation update) Myc protein (dMyc1) (dMyc) (Diminutive protein). Name-dm; ORFNames=C010798; Drosophila melanogaster (Fruit fly). Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
        GO; GO:0008810; F:cellulase activity; IEA.
GO; GO:0005975; P:carbohydrate metabolism; IEA.
InterPro; IPR001701; Glyco_hydro-9.
InterPro; IPR008928; Glyco_hydro-910.
InterPro; IPR008928; Glyco_trans_6hp.
InterPro; IPR008566; Lipocln_cytFABP.
Pfam; PF0759; Glyco_hydro-9; 1.
PROSITE; PS00592; GLYCOSYL_HYDROL_F9-1; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9-2; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9-2; 1.
PROSITE; PS00698; GLYCOSYL_HYDROL_F9-2; 1.
SEQUENCE 609 AA; 63618 MW; 7885B357203351A3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schreiber-Agus N., Stein D., Chen K., Goltz J.S., Stevens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the diminutive phenotype.";
Proc. Natl. Acad. Sci. U.S.A. 94:1235-1240(1997).
                                                                                                                                                                                                                                                                Score 54; DB 2;
Pred. No. 63;
                                                                                                                                                                                                                                                   33.5%; Scc. 56.2%; Pred. No. 00,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               717 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                                                                                                                                              451 ANOAYPAPNNAGTVYY 466
                                                                                                                                                                                                                                                                                                                                          2 ANRKOPKPNNSSTAYY 17
                                                                                                                                                                                                                                             Query Match
Best Local Similarity 56.2.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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MEDLINE=21850511; PubMed=11862395;
Miller K.M., Kaukinen K.H., Schulze A.D.;
"Expansion and contraction of major histocompatibility complex genes:
                                    Gaps
                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MHC class 1a antigen (Fragment)
Gadus morhua (Atlantic cod).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Paracanthopterygii; Gadiformes; Gadidae; Gadus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3,
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                                  Indels
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Last annotation update)
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Pred. No. 25;
6; Mismatches 10
              Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a teleostean example.";
Immunogenetics 53:941-953(2002).
EMBL, AF44217; AAL14543.1; -.
GO, GO:0016020; C:membrane; IEA.
GO, GO:0005955; P:immune response; IEA.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR00139; MIC_I.
Pfam; PF00159; MIC_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240 KRHKPDDSDTSSENTEGQKLAPEYQP 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5 KQPKPNNSSTAYYNFTGVSILPSYKP 30
                                                                                              135 PNNSSIRYLTKYGFTSVATHPNY 157
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                                                                     9 PNNSSTAY---YNFIGVSILPSY 28
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52.2%; Pre.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-1999 (TrEMBLrel. 10,
01-MAY-1999 (TrEMBLrel. 10,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS; PRO1638; MHCCI, 1.
PRINTS; PRO1638; MHCCLASSI.
SMOAT; SMO407; IGC1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas sp. YD-15.
Bacteria; Proteobacteria.
NCBI_TaxID=72609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 38.5
nes 10; Conservative
          Best Local Similarity 52.2
Matches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                        PRELIMINARY;
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Q95161;
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                                                                                                                                         DEVELOPMENTAL STAGE: Expressed both maternally and zygotically in
cellular blastoderm formation, particularly concentrated in pole plasm. Zygotic expression detected during cellular blastoderm stage in endodermal anlagan of anterior and posterior midgut at both poles. After gastrulation, expression detected in invaginating ventral furrow of mesoderm. Continued expression in anterior and posterior midgut and mesoderm during germband extension. During late germ-band retraction, expression remains detectable in fusing midgut and presumed developing somatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                             embryos.
-!- SIMILARITY: Contains 1 basic helix-loop-helix (bHLH) domain.
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Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Length 717;
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N -> S (in Ref. 3).
S -> K (in Ref. 3).
NNKLK -> IKNNN (in Ref. 3).
W, D6A74CF5D4B80150 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50888; Him; 1.
Activator; Coiled coil; DNA-binding; Nuclear protein;
Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase, FBgn0000472; dm.
GO; GO:0003700; F:transcription factor activity; IDA.
InterPro; IPR001092; HIM_basic.
Pfam; PF00110; HIM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helix-loop-helix motif.
Coiled coil (Potential)
Asn-rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      304 AA.
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Pred. No. 76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 ANRKOPKPNNSSTAYYNFIGVSILPSYKP 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Basic motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22484998; PubMed=12597275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bradyrhizobiaceae; Bradyrhizobium
                                                                                                                                                                                                                                                                                                                           EMBL, U77370; AAB39842.2; -... EMBL, U81384; AAD00517.1; -... EMBL, AE004427; AAF45866.2; -... EMBL; AL121800; CAD247801; -... EMBL; AY058627; AAL13856.1; -... EMSP; P25912; INLW.
                                                                                                                                                                                        79307 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OrderedLocusNames=bl16016;
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377
608
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362
365
373
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369
317 AA;
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Best Local Similarity
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STRAIN=USDA110;
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                                                                                                                               musculature.
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CONFLICT
SEQUENCE
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Gaps

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Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S., Madupu R., Melson W.C., Sullivan S.M., Fouts D.E., Haft D.H., Selengut J., Peterson J.D., Davidson T.M., Zafar N., Zafar N., Zhou L., Radme D., Dimitrov G., Hance M., Tran K., Khouri H.M., Gill J., Utterback T.R., Reldblyum T.V., Wall J.D., Voordouw G., Fraser C.M.; The genome sequence of the anaerobic, sulfate-reducing bacterium Desulfovibrio valgaris Hildenborough."; Bite Journal J. 22:554-559 (2004).

R. Bite J. AEO17317; AAS96997.1; -

R. TIGR; DVUZ515; -

R. InterPro; IPR003607; MeL_phos_hydro.

R. Pfam; PR01566; HD; I.

R. SMRT; SM0471.HD; 1.
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                                                                                                                                                                                                                                                                                                                                                            351 AA; 39994 MW; EB3DE1E08A05E58C CRC64;
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27-APR-2004 (TrEMBLrel. 27, Last sequence update)
11-MAY-2004 (TrEMBLrel. 27, Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                    32.9%; Score 53; DB 2; 39.3%; Pred. No. 47;
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Pred. No. 47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 KQPKPNNSSTAYYNFTG--VSILPSYKP 30
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24,
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Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                      Complete proteome. SEQUENCE 351 AA;
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01-JUN-2003
01-MAR-2004
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Q86128;
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AAS 96897
AC AAS 96
AC AAS 96
AC AAS 96
DT 27-API
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DT 11-MA
DE HU GG
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Q86128
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PubMed=1507118; DOI=10.1038/nbt959;
Heidelberg J.F., Seehadri R., Haveman S.A., Hemme C.L., Paulsen I.T.,
Kolonay J.F., Eisen J.A., Ward N.L., Methe B.A., Brinkac L.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombinant merozoite to Eimeria necatrix.";
                                                                                                                                                                                                                                                                                                                                                            Gaps
                Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
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..., Uchiumi T.,
..., Iriguchi M., Kawashima K.,
..., snimpo S., Tsuruoka H., Wada T., Yamada I.
Bradyrhischium japonicum USDA110.";
EMBL; AP005957; BAC51281.1;
InterPro: DR065628; GspK.
Pfam; PF03334; GspK; 1.
Complete protecome.
SEQUENCE 304.
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                                                                                                                                                                                                                                                                                                            2; Length 304;
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                                                                                                                                                                                                                                                                                                                                                         12; Indels
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Tajima O., Onaga H., Nakamura T.;
An enzyme-linked immunosurbent assay with the recombir
protein as antigen for detection of antibodies to Eimer
Avian Dis. 47:309-38(2003).
EMBL; AB070239; BABS5126.1; -
SEQUENCE 321 AA; 34175 MW; 10CB1CA4E32C1999 CRC64;
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Last annotation update)
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
HD domain protein.
                                                                                                                                                                                                                                                                                                  DB .
                                                                                                                                                                                                                                                                                                            Score 53; DB 2
Pred. No. 40;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                    6 QPKPNNSSTAYYNFTGVSILPSYKP 30
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ANRREKKPDTPAAAIYDFVG 128
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01-UUN-2002 (TrEMBLrel. 21,
01-UUN-2002 (TrEMBLrel. 21,
01-UUN-2002 (TrEMBLrel. 21,
NPmz19 protein.
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Best Local Similarity
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Best Local Similarity
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Q8TA73
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                                                                                                                                                                                                                    Gloeckner G., Eichinger L., Szafranski K., Pachebat J., Dear P., Lehmann R., Baumgart C., Parra G., April J.F., Guigo R., Kumpf K., Tungal B., Cox E., Quail M.A., Platzer M., Rosenthal A., Noegel A.A.; "Sequence and analysis of chromosome 2 of Dictyostelium discoideum."; Nature 418:79-85 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; MEDLINE=22608415; PubMed=12721630; DOI=10.1038/nature01582; Ivanova N., Sorokin A., Anderson I., Galleron N., Candelon B., Kapatral V., Battacharyya A., Reznik G., Mikhailova N., Lapidus A., Chu L., Mazur M., Goltsman E., Larsen N., D'Souza M., Walunas T., Grechkin Y., Pusch G., Haselkorn R., Fonstein M., Ehrlich S.D., Overbeek R., Kyrpides N.C.; Gerous and comparative analysis with Bacillus anthracis.";
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Similar to Dictyostelium discoideum (Slime mold). MkpA protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.9%; Score 53; DB 2; Length 411; Best Local Similarity 43.5%; Pred. No. 56; Matches 10; Conservative 5; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baumgart C.;
Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AC116305; AAO52322.1; -.
SEQUENCE 411 AA; 46427 MW; A0974D03F43FB6F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus cere" (strain ATCC 14579 / DSM 31).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBL_TaxID=226900;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 423:87-91(2003).
EMBL; AE016999; AAP07521.1; -.
INTECPPO; IPRO01466; Beta_lactamase.
Pfam; PF00144; Beta_lactamase; 1.
SEQUENCE 423 AA; 47619 MW; 19ABF50A949B37E9 CRC64;
               Dictyostalium discoideum (Slime mold).

Bukaryota, Mycerozoa, Dictyosteliida, Dictyostelium.

NCBI_TaxID=44669;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Penicillin-binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 27, Created)
(TrEMBLrel. 27, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     423 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 TAFFNFTNSNVKFSDCSIPSYKP 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                      STRAIN=AX4;
MEDLINE=22092622; PubMed=12097910;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 ANKEQQVPNNSETTFY 160
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                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                              SEQUENCE FROM N.A.
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05-JUL-2004
05-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=AX4;
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Q70H33
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10811818
AC 081181
DT 01-JU
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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE VARN Bangladesh B22R orthologue.

GN Name=fp9.123;

OS Viruses; daDNA virus (isolate HP-438[Munich]).

OC Viruses; daDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OX NCBI_TaxID=10263;

RN | SEQUENCE FROM N.A.

RA SKinner M.A. Laidlaw S.M.;

RA SKinner M.A. Laidlaw S.M.;

RY "Comparison of the genome sequence of FP9, an attenuated, tissue culture-adapted European twippox virus, with those of virulent

RT American and European viruses.";

RI J. Gen. Virol. 85.305-322(2004).

DR RNEL; AJS81527; CAE52664.1;

DR RNEL; AJS81527; CAE52664.1;

DR RNEL; AJS81527; CAE52664.1;

DR RNEL; AJS81527; CAE52664.1;

DR FROSTIE; PROUCHS B22R.

DR PROSTIE; PROUCHS B22R.

DR PROSTIE; PROUCHS B22R.

DR PROSTIE; PROUCHS B22R.

Query Match

Query Match

Query Match

RENNSSIAVRFITGVSILPSYKP 30

RENNSSTAYNFTGVSILPSYKP 30

B KRNNSSTAYNFTGVSILPSYKP 30

COS SEATCH Completed: November 10, 2004, 15:53:32

Search completed: November 10, 2004, 15:53:32
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Sequence 11674, A Sequence 1430, App Sequence 18475, App Sequence 19066, A Sequence 19965, A Sequence 251, App Sequence 268, App Sequence 261, App Sequence 265, App Sequence 64, Appl Sequence 64, Appl Sequence 64, Appl

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Sequence 22, Application US/09097889
Fatent No. 621817
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Davis, Robert B.
ITILE OF INVENTION: COMPOSITIONS AND METHODS FOR IDENTIFYING
TITLE OF INVENTION: EXTRAMITOCHONDRIAL DNA: MITOCHONDRIAL DNA RATIOS
INUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA

ZIF: 98104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATA:
COMPUTER: IBM PC COMPATA:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/097,889
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROSSIMEN Ph.D., Stephen J.
REGISTRATION NUMBER: 660088.417
TELESTANTION NUMBER: 620088.417
US-09-489-039A-11674

US-09-248-796A-130

US-09-248-796A-19966

US-09-248-796A-19966

US-09-248-796A-19966

US-09-248-796A-19966

US-09-248-796A-19965

US-09-248-796A-19965

US-09-577-304A-251

US-09-577-304A-251

US-09-577-304A-268

US-09-577-304A-268
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87.5%; Pred. No. 0.00019;
Live 1; Mismatches 1;
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amino acid
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Best Local Similarity 87.5
Matches 14; Conservative
    CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
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US-09-097-889-22
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                                                                                                                                                    November 10, 2004, 14:55:47; Search time 7.40214 Seconds (without alignments) 143.349 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Issued Patents AA:*
1: /cgn2_6/ptodate/1/iaa/5A_COMB.pep:*
   /cgn2_6/ptodate/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-097-889-22
US-09-187-959-6
US-09-187-859-6
US-09-187-859-6
US-08-188-282-6
US-08-135-852-6
US-08-332-643-44
US-08-332-643-44
US-09-248-796A-1466
US-09-248-796A-1466
US-09-246-796A-1466
US-09-246-796A-14108
US-09-270-767-52191
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US-09-508-691-5
US-09-540-236-2212
US-09-602-787A-478
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Maximum Match 1008
Listing first 45 summaries
                                                                                                                    protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                   BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                     US-10-092-750-70
85
1 GSLTHHINNIKPSSTR 16
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                       Title:
Perfect score:
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                                                                                                                                                                 Run on:
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                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09187859A

Sequence 6. Application US/09187859A

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
APPLICANT: Blaschuk, Orest W.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL
TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.4070.1
CURRENT RILING DATE: 1998-11-06
NUMBER OF SEQ ID NOS: 4052
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO S.
SEQ ID NO S.
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Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                4; Indels
                                                                                                                                                                          DB 4;
                                                                                                                                                                      Score 47; DB 4
Pred. No. 3.4;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-839-542B-6; Sequence 6, Application US/09839542B; Patent No. 6569996; BREAL INFORMATION:
                                                                                                                                                                               55.3%;
69.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 SLTHHINNIKPSSTR 16
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; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27380
                                                                                                                                                                                                                                                                                                                                                                                                                                               36 SYTHHSNNHKPQS 48
                                                                                                                                                                                                                                                                                                                                                          2 SLTHHINNIKPSS 14
                                                                                                                                                                          Query Match
Best Local Similarity 69.2
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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; ORGANISM: Homo sapiens
US-09-839-542B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 8; Conserv
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US-09-187-859-6
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Sequence 27380, Application US/09248796A

Sequence 27380, Application US/09248796A

Sequence 27380, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUMBER: US/09/248,796A

FILE REFERENCE: 107196-112

FILE REFERENCE: 107196-112

PRIOR PELING DATE: 1998-02-12

PRIOR PILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

LENGTH: 163
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                                                                                                                                                                                                                                                                                                      DEBLICANT: Herrnstadt, Corrina
APPLICANT: Herrnstadt, Corrina
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Fahy, Boin F.
TITLE OF INVENTION: DIAGNOSTIC METHOD BASED ON QUANTIFICATION OF
TITLE OF INVENTION: EXTRAMITOCHONDDRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seatile
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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89.4%; Score 76; DB 4; Length 459;
Best Local Similarity 87.5%; Pred. No. 0.00019;
Matches 14; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: COMPUTER: IBM PC compatible
COMPUTER: CO
                                                                                                                                                                          Sequence 22, Application US/09098079 Patent No. 6489095 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GSLTHHINNIKPSSTR 16
                                                                                                   RESULT 2
US-09-098-079-22
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                                                                        Score 42; DB 1; Length 780;
Pred. No. 1.2e+02;
2; Mismatches 5; Indels
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Pred. No. 1.2e+02;
Sredis 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:

LIP: 60603

ZIP: 60603

CONTINENT READABLE FORM:

MEDIUW TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM:

OPERATING SYSTEM:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

CLASSITCATION NUMBER: US/08/332,643

FILING DATE:

APPLICATION NUMBER: US/08/332,643

FILING DATE:

APPLICATION NUMBER: US/07/972,643

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: NO. 539363443, Geta E.

REGISTRATION NUMBER: 27866/30795

REFERENCE/DOCKET NUMBER: 27866/30795

TELECOMMUNICATION INFORMATION:

MET STATUM NUMBER: 35,302

REFERENCE/DOCKET NUMBER: 27866/30795
                                                                                                                                                                                                                                                                           ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Bicknell STREET: Two First National Plaza, 20 South Clark STREET: Street CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-08-312-638-50
Squence 50, Application US/08332638
Patent No. 5646250
GENERAL INFORATION:
APPLICANT: Subuki, Shintaro
ITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 780 amino acids
TYPE: amino acid
                                                                          Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative 5
                                                                                                                                                                      2 SLTHHINNIKPSSTR 16
                                                                                                                                                                                                            59 SLPHHVGKIKSSVSR 73
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       ; MOLECULE TYPE: protein US-08-188-228-50
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US-09-535-852-6;
Sequence 6, Application US/09535852;
Patent No. 6638911
GENERAL INFORMATION:
APPLICANT: Blachuk, Orest W.
APPLICANT: Blachuk, Orest W.
TITLE OF INVENTION: DESWOSCHAL CADHERIN-MEDIATING
TITLE OF INVENTION: DESWOSCHAL CADHERIN-MEDIATED FUNCTIONS
FILE REFERENCE: 100086.407C6;
CURRENT PILING DATE: 2010-05-21
NUMBER OF SEQ ID NOS: 2009
SEQ ID NO 6
LENTER FALSE FASEED for Windows Version 4.0
LENTER FOR THE NO 6
LENTER FASEED FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
49.4%; Score 42; DB 4; Length 108;
Best Local Similarity 53.3%; Pred. No. 14;
Matches 8; Conservative 2; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 50, Application US/08188228;
Patent No. 5597725;
GENERAL INFORMATION:
APPLICANT: SULKI, SHINTARO
TITLE OP INFORMATION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Barun
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIPRCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US 07/872,643
FILING DATE: UN DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: US 07/872,643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SLTHHINNIKPSSTR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-188-228-50
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-535-852-6
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                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Lan, Michael S.
APPLICANT: No. 6225049kins, Abner L.
TITLE OF INVENTION: NOVEL HUMAN INSULINOMA-ASSOCIATED CDNA
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB 3; Length 510;
Pred. No. 1.1e+02;
0; Mismatches 6; Indels
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Sequence 7482, Application US/09621976
Patent No. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REPERENCE: GARSET. 054PRA
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Flappy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive CITY: Newport Beach STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PILING DATE:
CLASSIFICATION DATA:
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMER: US/07/901,715
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER: NIH012.012A
TELECOMUNICATION INFORMATION:
TELEPACNE: (619) 235-650
TELEPACNE: (619) 235-6176
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            Sequence 2, Application US/08246489 Patent No. 6225049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative (
                                                                   153 GSITHTVIENKPSSS 167
                              1 GSLTHHINNIKPSST 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 510 amino acids
amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
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J Sequence 14668, Application US/09248796A

J Sequence 14668, Application US/09248796A

J Sequence 14668, Application US/09248796A

J Sequence No. 6747137

GENERAL INFORMATION:

J TILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

TILLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR PELING DATE: 1999-02-13

PRIOR PELING DATE: 1999-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 14668

LENGTH: 271
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Best Local Similarity 53.3%; Pred. No. 56;
Matches 8; Conservative 3; Mismatches 4; Indels
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                                                                                                                                                                                                                                  CONDURY: USACOUNTRY: USACOUNTR
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & ADDRESSEE: Borun
STREET: 6310 Sears Tower, 233 S. Wacker Drive CITY: Chicago STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 SLIHHINNIKPSSIR 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Candida
US-09-248-796A-14668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-332-638-50
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US-09-270-767-36974
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PIREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 14108
LENGTH: 63
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Sequence 5518, Application US/09513999C

Setent No. 6783961

GENERAL INFORMATION:

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.;

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

FILE REPERENCE: 59,US2.REG

CURRENT FILING DATE: 2000-02-24

FRIOR PELING DATE: 1999-02-26

NUMBER: OF SEQ ID NOS: 36681

SOFTWARE: Patent.pm

SEQ ID NO 5518

LENGTH: 128

WANDER OF SEG ID NOS: 36681

SOFTWARE: PATENT PRINTED TO SEG ID NOS: 36681

SEQ ID NO 5518
                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 47.1%; Score 40; DB 4; Length 63; Best Local Similarity 60.0%; Pred. No. 16; Matches 6; Conservative 3; Mismatches 1; Indels
                                                                                                                                                                         Length 50;
                                                                                                                                                                                                                     Indels
                                                                                                                                                                       Ouery Match
Best Local Similarity 30.0%; Pred. No. 13;
Matches 9; Conservative 4; Mismatches
                                                                                                                                                                                                                                                                                         --NNIKPSSTR 16
                                                                                                                                                                                                                                                                                                                                                                 RESULT 13
US-069-489-039A-14108
; Sequence 14108, Application US/09489039A
; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Klebsiella pneumoniae
; NUMBER OF SEQ ID NOS: 19335; SOFTWARE: Patent.pm; SEQ ID NO 7482
; LENGTH: 50; TYPE: PRT; TYPE: PRT; ORGANISM: Home sapiens
US-09-621-976-7482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 LTHHINNIKP 12
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41 ITHYVNNGKP 50
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US-09-513-999C-5518
                                                                                                                                                                                                                                                             3 LTHHI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-489-039A-14108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-513-999C-5518
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RESULT 15

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BESULT 15

US-09-270-767-36974

Sequence 36974, Application US/09270767

Sequence 36974, Application US/09270767

Sequence 36974, Application US/09270767

SEQUENCE SEQUENCE: File Reference: 7326-094

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster TITLE OF INVENTION: NUMBER: US/09/270,767

CURRENT PELING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SEQ ID NO 36974

SEQ ID NO 36974

CURRENT PRING PARCH

SEQ ID NO 36974

MARCHES PRINGING

OPEN MARCH

GHINNIRPSSIR 16

SEA LOCAL Similarity 54.5%; Pred: No. 47;

Batches 6; Conservative 3; Mismatches 2; Indels 0; Gaps O; Matches 6; Conservative 3; Mismatches 2; Indels O; Gaps O; Db Li3 HINNIRPSYIR 133

Search completed: November 10, 2004, 15:57:22

Job time: 8.40214 secs
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Run on:

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Sequence 52425, A Sequence 31950, A Sequence 213418, Sequence 1211, App Sequence 1211, App Sequence 1211, App Sequence 1211, App Sequence 239832, Sequence 239832, Sequence 2220, App Sequence 2520, App Sequence 242398, Sequence 2520, App Sequence 2520, App Sequence 2520, App Sequence 2520, App Sequence 25, App I Sequence 25, App I Sequence 25, App I Sequence 23, App I Sequence 24, App I Sequence 25, App I Sequ
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Sequence 45,
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JS-Quance 70, Application US/10092750

PUDLICATION NO. US20030032157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Alpin, Julia

APPLICANT: Wright, Martin C.

ITILE OF INVERTION: POlypeptides Interactive with BCL-X1

FILE REFERENCE: 50036/050002

CURRENT FILENG DATE: 2002-03-07

PRIOR APPLICATION NUMBER: US/10/092,750

CURRENT PILING DATE: 2001-03-08

MUMBER: OF SEQ ID NOS: 233

SOFTWARE: FastSEQ for Mindows Version 4.0

SEQ ID NO 70

LENGTH: 16

TUDDE: NOR THE CONTRACTION NUMBER: US/10/092/1510

SEQ ID NO 70

LENGTH: 16

TUDDE: NUMBER: US/10/092/1510

SEQ ID NO 70

LENGTH: 16
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5 US-10-424-599-256084

5 US-10-424-599-184641

5 US-10-425-114-36475

7 US-10-425-114-36276

6 US-10-426-114-36277

105-10-426-114-36277

105-10-408-765A-74

105-10-408-765A-74

105-10-408-765A-74

105-10-408-765A-74

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105-10-418-8
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100.0%; Pred. No. 8.4e-07;
tive 0; Mismatches 0;
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US-10-425-115-336967
; Sequence 336967, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GSLTHHINNIKPSSTR 16
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Les 16; Conservative
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US-10-092-750-70

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Matches
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Sequence 22, Appl
Sequence 22, Appl
Sequence 36, Appl
Sequence 282, Appl
Sequence 282, Appl
Sequence 278981,
Sequence 278981,
Sequence 53894,
Sequence 53894,
Sequence 53894,
Sequence 53894,
Sequence 53894,
Sequence 258437,
Sequence 258437,
                                                                                                                                       November 11, 2004, 02:43:24; Search time 38.6619 Seconds (without alignments) 146.426 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Published Applications AA:*

1: /cgm2_6/prodata/2/pubpaa/PCT_PW PUBCOMB.pep:*

2: /cgm2_6/prodata/2/pubpaa/PCT_PW PUB.pep:*

4: /cgm2_6/prodata/2/pubpaa/NCG_NEW PUB.pep:*

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7: /cgm2_6/prodata/2/pubpaa/USOF_NEW PUB.pep:*

8: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

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11: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

12: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

13: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

14: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

15: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

16: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

17: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

18: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

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19: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*

10: /cgm2_6/prodata/2/pubpaa/USOF_PUBCOMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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17 US-10-425-115-33-967

18 US-09-098-487-36

16 US-10-428-487-36

16 US-10-408-765A-1

15 US-10-408-765A-2682

15 US-10-428-599-28892

15 US-10-437-963-111254

15 US-10-437-963-11254

17 US-10-425-115-256437

16 US-10-425-115-256437

16 US-10-425-115-256437

16 US-10-425-963-115-256437

17 US-10-425-963-115-256437

18 US-10-425-963-115-256437

19 US-10-424-599-225540
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                                                                                                                                                                                                                                                                                                                                                                            1568699 seqs, 353819137 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                      - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                       US-10-092-750-70
85
1 GSLTHHINNIKPSSTR 16
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                                                                                                                                                                                Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score
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                                                                                                                                                                                                                                                                        Sequence:
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Publication No. US20040006780A1

GENERAL INFORMATION:

APPLICANT: RASTELL, LUCA K.

APPLICANT: RASTELL, LUCA K.

TITLE OF INVENTION: VECE-MODULATED GENES AND METHODS EMPLOYING THEM

FILE REFERENCE: 09800080-0103

CURRENT' APPLICATION NUMBER: US/10/428,487

CURRENT' APPLICATION NUMBER: 09/815,153

PRIOR APPLICATION NUMBER: 60/191,201

PRIOR FILING DATE: 2000-03-22

NUMBER OF SEQ ID NOS: 84

SOSTWARE: Patentin Ver. 2.1

SEQ ID NO 36

LENGTH: 459
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APPLICANT: Zhang, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glosm, Gary M.
APPLICANT: Warnock, Dale B.
TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE REPRENCE: 660089.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DAIR: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH 459
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                                        Query Match

89.4%; Score 76; DB 9; Length 459;
Best Local Similarity 87.5%; Pred. No. 0.00086;
Matches 14; Conservative 1; Mismatches 1; Indels
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89.4%; Score 76; DB 16; Length 45
Best Local Similarity 87.5%; Pred. No. 0.00086;
Matches 14; Conservative 1; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    417 GSLTHHINNMKPSFTR 432
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                                                                                                                                                      1 GSLTHHINNIKPSSTR 16
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US-10-408-765A-1
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US-10-428-487-36
                                                                                                                                                                                                                                                                                 RESULT 4
US-10-428-487-36
US-09-098-079-22
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  APPLICANT: La Rosa, Thomas J.
APPLICANT: Xovalic, David K.
APPLICANT: Xovalic, David K.
APPLICANT: Anou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21(5322)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 336967
LENGTH: 114
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Sequence 22, Application US/09098079

Patent No. US20020064773A1

GENERAL INFORMATION:
APPLICANT: Herneradt, Corrina
APPLICANT: Clevenger, William
APPLICANT: Clevenger, William
APPLICANT: Davis, Nobert S.
APPLICANT: Pahy, Boin F.
TITLE OF INVENTION: EXTRAMITCHONDBRIAL DNA
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS: 36
CORRESPONDENCE ADDRESS: 36
CORRESPONDENCE ADDRESS: 46
CORRESPONDENCE ADDRESS: 46
CORRESPONDENCE ADDRESS: 46
COURTY: Seattle
STATE: Washington
CITY: USA
COUNTRY: USA
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CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/098,079
FILING DATE: 15-JUN-1998
CLASSIFICATION: 435
ATTONENY/AGENT INPORMATION:
NAME: ROSENMEN Ph.D. Stephen J.
REGISTRATION NUMBER: 43,058
REPRENCE/DOCKET NUMBER: 660088.416
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF 22:
SEQUENCE CHRAACTERISTICS:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHRAACTERISTICS:
CHRAACTERISTICS:
SEQUENCE CHRAACTERISTICS:
STRANDENESS:
TOPOLOGY: linear
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US-10-425-115-336967
                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: unsure
LOCATION: (1)..(114)
OTHER INFORMATION: unsure at all Xaa locations
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COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ORGANISM: Zea mays
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US-09-098-079-22
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Sequence 111254, Application US/10437963
Fublication No. US20040123343A1
Fublication No. US20040123343A1
Fublication No. US20040123343A1
Fublication No. US20040123343A1
Fublication No. US2004012343A1
FublicANT: La Rosa, Thomas J.
FublicANT: Exp. Yibina
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 111254
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US-10-424-599-249656
US-10-424-599-249656
I Sequence 249656, Application US/10424599
I Sequence 249656, Application US/10424599
I Sequence 249656, Application No. US20040031072AI
I SEMERAL INFORMATION:
I APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwid K
APPLICANT: Cao Yongwid K
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
ITILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
I SEQ ID NOS: 285684
I SEQ ID NOS: 285684
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Pred. No. 27;
3; Mismatches 3; Indels
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US-10-424-599-249656
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US-10-437-963-111254
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OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Sest Local Similarity 60.0%; Pred. No. 4.8;
Matches 9; Conservative 3; Mismatches
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Best Local Similarity 57.1%;
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 GSLTYRIGSVSPSST 19
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34 SLSHRINAVKPSKT 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LAR ROSA Thomas J
APPLICANT: Lar Royalic David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Shou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 278981
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                                                                                                                                                                                                                                      APPLICANT: Ghosh, Soumitra S.
APPLICANT: Ghosh, Soin D.
APPLICANT: Tang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary W.
APPLICANT: Warnock, Dale E.
TILLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICANTION NUMBER: US/10/408,765A
CURRENT APPLICANTION NUMBER: 203-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-424-599-278981
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OTHER INFORMATION: unsure at all Xaa locations
                                                                                                                                                          Sequence 2682, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION:
417 GSLTHHINNMKPSFTR 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   417 GSLTHHINNMKPSFTR 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
US-10-408-765A-2682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Glycine max
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LENGTH: 459
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NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 258437
LENGTH: 42
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ORGANISM: Glycine max
                                                                                                                      TYPE: PRT
ORGANISM: Zea mays
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Yohua
APPLICANT: Cao, Yohua
APPLICANT: Cao, Yohua
APPLICANT: APPLICANT: APPLICANT: Diou, Yihua
APPLICANT: APPLICANT: Diou, Yihua
APPLICANT: Diou, Yihua
APPLICANT: Diou, Yihua
APPLICANT: Usono, Yohua
APPLICANT: Usono, Yohua
TITLE OF INVENTION: Plants
FILE REPERENCE: 38-21 (53222) B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANI: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFREENCE: ELITRA.034

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-05-23

PRIOR FILING DATE: 2000-05-23

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/207,727

PRIOR PLICATION NUMBER: 60/203,335

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR PILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-10-23

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PILING DATE: 2001-12-20

PRIOR PILING DATE: 2001-02-16

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                                                                         Sequence 53894, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Mang, Liangsu
APPLICANT: Malon, Carlos
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Oblsen, Kari
APPLICANT: Cybind, Judith
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; ORGANISM: Cornyebacterium diptheriae
US-10-282-122A-53894
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                                                                                                                                                                                                                                                                                                                                                                                                                   Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
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Matches 9, Conservative
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GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: Rovalic, David K.
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Size Nucleic Acid Molecules and Other Molecules Associated
APPLICANT: Size Nucleic Acid Molecules and Other Molecules
APPLICANT: Size Nucleic Acid Molecules
APPLICANT: Applicant
APPLICANT: Size Nucleic Acid Molecules
APPLICANT: Size Nucleic Acid Molecules
APPLICANT: Applicant
APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT: And APPLICANT
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Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yould David K
APPLICANT: Cao Yougwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: 2003-04-28
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 225540
LENGTH: 314
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                                                                                                                                          Score 44; DB 17; Length 42;
Pred. No. 9.6;
1; Mismatches 5; Indels
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CTHER INFORMATION: Clone ID: PAT_MRT4530_84915C.1.pep
US-10-437-963-188297
, OTHER INFORMATION: Clone ID: MRT4577_167281C.1.pep
US-10-425-115-258437
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Pred. No. 82;
2; Mismatches 3;
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Best Local Similarity 61.5%;
Matches 8; Conservative 7
                                                                                                                                              Query Match
Best Local Similarity 60.0%;
Matches 9; Conservative
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Search completed: November 11, 2004, 07:41:46 Job time : 38.6619 secs
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Sequence 256084, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Acvalic David K
APPLICANT: Acvalic David K
APPLICANT: Acvalic David K
APPLICANT: Cac Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO S: 285684
SEQ ID NO S: 285684
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Sequence 184641, Application US/10424599;
Publication No. US20040031072A1
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Pred. No. 83;
1; Mismatches 2; Indels
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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_45694C.1.pep
US-10-424-599-225540
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US-10-424-599-256084
                                                                                                                                                                              Query Match
Best Local Similarity 72.7%;
Matches 8; Conservative
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262 LTHHIYNLGPGS 273
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114 STTNHINNISP 124
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ORGANISM: Glycine max
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US-10-424-599-256084
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3 LTHHINNIKPSS 14

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model

November 10, 2004, 14:52:32; Search time 5.46619 Seconds (without alignments) 281.634 Million cell updates/sec Run on:

US-10-092-750-70 85 1 GSLTHHINNIKPSSTR 16

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	NADH2 dehydrogenas		NADH2 dehydrogenas								NADH2 dehydrogenas					-		σ	σ	יסי מי	NADH2 dehydrogenas								
SUMMARIES	ID	A00435	DNHUN4	T17141	QXG14M	A00437	A00436	A59154	T11372	T11866	T11256	B58851	T10981	T11059	T11502	S41829	QXBO4M	T11515	T11411	S41844	826160	S04756	177325	177323	177321	177327	1713	1714	7	1715
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d	Query Match	89.4	σ _ν	85.9	78.8	7	ů.	9	9	9		'n.	72.9			ö	69.4	69.4	ď	68.2	æ	æ	ď.	'n	62.9	'n.	'n.	ů.	ů.	'n
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44 44 RV RV RV RV RV RV	4 4 4 0 0 0 0			152	
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30 31 32 55				43	

ALIGNMENTS

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - chimpanzee mitochondrion (fragm N,Alternate names: NADH-ubiquinone oxidoreductase chain 4 (Species: mitochondrion Pan troglodytes (chimpanzee) C,Species: mitochondrion Pan troglodytes (chimpanzee) C,Accession: A00435 (Arager, E.M.; Wang, A.; Wilson, A.C. J. AODI-2004 (A. Frager, E.M.; Wang, A.; Wilson, A.C. J. AODI-2004 (A. Frager, E.M.; Wang, A.; Wilson, A.C. J. AODI-2004 (A. Frager, E.M.; Wang, A.; Wilson, A.C. J. AODI-2004 (A. Frager, E.M.; Wang, A.; Wilson, A.C. J. AODI-2004 (A. Frager, E.M.) AODI

ö Gaps ; 0 Query Match 89.4%; Score 76; DB 2; Length 152; Best Local Similarity 87.5%; Pred. No. 1.5e-05; Matches 14; Conservative 1; Mismatches 1; Indels

110 GSLTHHINNMKPSFTR 125 1 GSLTHHINNIKPSSTR 16 ઠ ద

NADR2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - human mitochondrion N'Alternate names: NADH-ubiquinone oxidoreductase chain 4 c;Species: mitochondrion Homo sapiens (man) C;Date: 22-May-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004 C;Accession: A00434; B00435 R;Anderson, S.; Bankier, A.T.; Barrell, B.G.; de Bruijn, M.H.L.; Coulson, A.R.; Drouin,

Nature 290, 457-465, 1981

Agrithe: Sequence and organization of the human mitochondrial genome.

A; Fitle: Sequence and organization of the human mitochondrial genome.

A; Reference number: A00151; MUID:81173052; PMID:7219534

A; Accession: A00434

A; Accession: A00434

A; Residues: 1-459 cAND

A; Residues: 1-459 cAND

A; Residues: 1-459 cAND

A; Residues: UNIPROT:P03905; GB:J01415; GB:M12548; GB:M58503; GB:M639393; Rown, W. M. A; Prager, E. M.; Wang, A.; Wilson, A.C.

J; Monow, W. M.; Prager, E. M.; Wang, A.; Wilson, A.C.

J; Mol. Evol. 18, 225-239; 1982

A; Title: Mitochondrial DNA sequences of primates: tempo and mode of evolution.

A; Reference number: A00435; MUID:82242101; PMID:6284948

A; Molecule type: DNA

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Nuclear dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - orangutan mitochondrion (fragmen NiAlternate names: NADH-ubiquinone oxidoreductase chain 4
C.Species: mitochondrion Pongo pygmaeus (orangutan)
C.Species: mitochondrion Pongo pygmaeus (orangutan)
C.Accession: A00437
R.Brown, W.M.; Prager, E.M.; Wang, A.; Wilson, A.C.
J. Mol. Broll 22-239, 1982
A.Fitle: Mitochondrial DNA sequences of primates: tempo and mode of evolution.
A;Reference number: A00435; MUD:82242101; PMID:6284948
A;Accession: A00437

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A;Genome: mitochondrion
A;Genetic code: SGC1
A;Note: NADH4
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Steywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A,Genetic code: SGCI
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Genetic code: SGCI
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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417 GTLTHHIKNMKPSLTR 432
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A;Molecule type: DNA
A;Residues: 1-152 <BRO>
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - common gibbon mitochondrion (fra c) Species mitochondrion Hylobates lar (common gibbon, white-handed gibbon)
C; Date: 17-Dec-1982 #sequence_revision 26-Aug-1999 #text_change 09-Jul-2004
C; Accession: T1842; A00438
R; Arnason, U; Gullberg, A; Xu, X.
Heredites 124, 185-189; 1996
A; Title: A complete mitochondrial DNA molecule of the white-handed gibbon, Hylobates lar A; Reference number: 217353
A; Accession: T1842
A; Reference number: 217353
A; Accession: T1842
A; Residues: 1-459 cARN
A; Residues: 2004456; MID:82242101; PMID:6284948
A; Residues: 308-459 cBRO
A; Tritle: Mitochondrial DNA
A; Residues: 308-459 cBRO
A; C; Genetics: 2008-459 cBRO
C; Genetics: 2008-459 cBRO
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R; Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xi
R; Wang, W.; Forstner, M.R.J.; Zhang, Y.P.; Lui, Z.M.; Wei, Y.; Huang, H.Q.; Hu, H.G.; Xi
Int. J. Primatol. 18, 305-320, 1997

A; Primatol. 18, 305-320, 1997

A; Reference number: Z18709

A; Accession: T1714

A; Accession: T1714

A; Residues: DNA

A; Residues: 1-459 < WAN

A; Residues: 1-459 < WAN

A; Cross-references: UNIPROT: O21697; EMBL: U92950; NID: G2290413; PID: G2290416; PIDN: AAD046

C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4

C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
A; Residues: 308-459 <BRO>
A; Cross-references: GB:L00016; EMBL:V00658; NID:g337302
A; Note: this ORF is not annotated in GenBank entry HUMMTTRPR, release 106
C; Genetics:
A; Gene: GDB:MTND4
A; Gene: GDB:MTND4
A; Gene: GDB:I18914; OMIM:516003
A; Gene: mitochondrion
A; Genome: mitochondrion
A; Generic code: SGCI
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Reywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C;Species: mitochondrion Colobus guereza (guereza)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
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85.9%; Score 73; DB 2; Length 459;
Best Local Similarity 87.5%; Pred. No. 0.00017;
Matches 14; Conservative 0; Mismatches 2; Indels
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PIDN: CAA5608

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RESULT 10
T11256
NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - greater Indian rhinoceros mitocl
C;Species: mitochondrion Rhinoceros unicornis (greater Indian rhinoceros)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T11256
R;Xu, X:; Janke, A.; Arnason, U.
Mol. Biol. Evol. 13, 1167-1173, 1996
A;Title: The complete mitochondrial DNA sequence of the greater indian rhinocerus, Rhin
                                                                                                                                                         horse, Equus caballus: Extensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g12772; PIDN:CAA43448.1; PID:g12780
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B58851
NADIAC dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - finback whale mitochondrion Cispecies: mitochondrion Balaenoptera physalus (finback whale, common rorqual) C;Species: mitochondrion Balaenoptera physalus (finback whale, common rorqual) C;Date: 14-Aug-1998 #text_change 09-Jul-2004 C;Accession: B5881, 1991
M;Arnason, U; Gullberg, A.; Widegren, B.
J. Mol. Evol. 33, 556-568, 1991
A;Title: The complete nucleotide sequence of the mitochondrial DNA of the fin whale, A;Recession: B58851
A;Accession: B58851
A;Molecule type: DNA
A;Residues: 1-459 cAEN>
A;Coss-references: UNIFROT: P24975; GB: X61145; NID: G12772; PIDN: CAA43448.1; PID: G12772; P
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A; Accession: T11256
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-459 < XUX>
A; Cross-references: UNIPROT:096068; EMBL:X97336; NID:g1666193; PIDN:CAA66010.1;
A; Experimental source: kidney
C; Genetics:
R;Xu, X.; Arnason, U.

Gene 148, 357-362, 1994
A;Title: The complete mitochondrial DNA sequence of the horse, Equus caball
A;Reference number: Z17369; MUID:95047450; PMID:7958969
A;Accession: T11866
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-459 <XUX>
A;Residues: 1-459 <XUX>
C;Genetics: C;Genetics: UNIPROT:P48655; EMBL:X79547; NID:g577571; PID:g577581;
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A;Genetic code: SGC1
C;Superfamily: NADH dehydrogenase (ubiquinone) chain
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76.5%; Score 65; DB 2;
Best Local Similarity 75.0%; Pred. No. 0.0038;
Matches 12; Conservative 1; Mismatches 3
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417 GKYTYHINNIKPSFTR 432
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Cipacies: mitochondrion Gorilla gorilla gorilla (western lowland gorilla)
Cipacies: mitochondrion Gorilla gorilla gorilla (cipacies)
Cipacies: Mitochondrion Gorilla Gorilla (western lowlange 09-Jul-2004
Cipacession: A59154
R; Xu, X.; Arnason, U.
Mol. Biol. Evol. 13, 691-698, 1996
A; Title: A complete sequence of the mitochondrial genome of the Western lowland gorilla.
A; Reference number: Z17269; MuID:96212991; PMID:8676744
A; Reference number: Movember 1995
A; Rocession: A59154
A; Residues: 1-459
A; Note: this translation is not annotated in GenBank entry GGMITG, release 114.0
A; Note: the termination resulting from transcript polyadenylation is shown
C; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
                                                                                                                                                                                                                        A59154
MDDA2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - western lowland gorilla mitochon NADPA2 dehydrogenase (ubiquinone oxidoreductase chain 4
C;Species: mitochondrion Gorilla gorilla gorilla (western lowland gorilla)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;McCession: A59154
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NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - horse mitochondrion C;Species: mitochondrion Equus caballus (domestic horse)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004 C;Accession: T11866
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ALLOWARD dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - dog mitochondrion (fragment) C, Species: mitochondrion Canis lupus familiaris (dog)
C, Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C, Accession: T11502
R, Kim, K.S.; Lee, S.E.; Jeong, H.W.; Ha, J.H.
Wol. Phylogenet. Evol. 10, 210-220, 1998
A, Tritle: The complete nucleotide sequence of the domestic dog (Canis familiaris) mitocho A, Reference number: Z17276; MUID:99097286; PMID:9878232
A,Accession: T11502
A,Accession: T11502
A,Accession: T11502
A,Residues: nucleic acid sequence not shown; translation not shown; translation of shown; translation
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A;Residues: 1-459 ARN>
A;Cross.references: UNIPROT:P41298; EMBL:X72204; NID:g414126; PIDN:CAA51004.1; PID:g4141
A;Note: the stop codon is generated by polyadenylation
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C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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A,Genetic code: SGC1
C,Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C,Keywords: membrane-associated complex, mitochondrion; NAD; oxidative phosphorylation;
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Pred. No. 0.027;
1; Mismatches 4; Indels
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                                      Length 459;
                                                                                                    4; Indels
                                  DB 2;
0.018;
                                                                                                       Mismatches
                                  Score 61;
Pred. No.
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                                  71.8%;
75.0%;
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Best Local Similarity 75.0
Matches 12; Conservative
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NADP12 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - pig mitochondrion
C,Species: mitochondrion Sus scrofa domestica (domestic pig)
C,Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C,Accesion: T10981; T11879
C,Date: 16-Jul-2099 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C,Accesion: T10981; T11879
C,Date: 10-Jul-2099 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C,Accesion: T10981
A,Description: Complete nucleotide sequence of the porcine mitochondrial genome.
A,Resference number: 27237
A,Accession: T10981
A,Residues: preliminary; translated from GB/EMBL/DDBJ
A,Residues: 1459 *LLN>
A,Residues: 1459 *LLN>
A,Residues: UASP *LNN>
A,Residues: INASP *LNN>
A,Residues: INASP *LNN>
A,Cross-references: UNIPROT: 079881; EMBL:AF034253; NID:g4958951; PID:g4958961; PIDN:AAD3
A,Cross-references: UNIPROT: 27370
A,Description: The complete mitochondrial DNA sequence of the pig (Sus scrofa).
A,Reference number: 217370
A,Reference number: 217370
A,Reference number: 217370
A,Reference number: 217370
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A;Molecule type: DNA
A;Molecule types: 1-459 <HIES
A;Residues: 1-459 <HIES
A;Cross-references: UNIPROT:078755; EMBL.AF010406; NID:g3445513; PID:g3445515; PIDN:AAD1
A;Experimental source: strain Merinolandschaf; liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MADDE dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - sheep mitochondrion MADDE dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 4 - sheep mitochondrion Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Species: mitochondrion Ovis orientalis aries, Ovis ammon aries (domestic sheep) C;Date: 16-Uul-1999 #sequence_revision 16-Uul-1999 #text_change 09-Uul-2004 R;Hiendleder, S.; Lewalski, H.; Wassmuth, R.; Janke, A. Mol. Evol. 47, 441-448, 1998 #Title: The complete mitochondrial DNA sequence of the domestic sheep (Ovis aries) and A;Reference number: Z17245; MUID:98440761; PMID:9767689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: witochondrion
A;Genetic code: SGCI
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
C; Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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C,Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C,Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;
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Pred. No. 0.012;
0; Mismatches 4; Indels
                                                                 ch 72.9%; Score 62; DB 2; Length 459; 1 Similarity 75.0%; Pred. No. 0.012; 12; Conservative 0; Mismatches 4; Indels
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A;Molecule type: DNA
A;Residues: 1-360,'V',362-427,'P',429-459,'C' <URS>
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A;Cross-references: EMBL:AJ002189; PIDN:CAA05237.1
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Matches 12; Conservative
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Search completed: November 10, 2004, 15:55:06 Job time : 5.46619 secs

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Q9b2x6 homo sapien Q9b2x8 homo sapien Q9b2y5 homo sapien Q9b2y7 homo sapien Q9b300 homo sapien Q8wcy0 homo sapien Q8wcy0 homo sapien Aa154419 homo sapi Aa15445 homo sapi Aa154478 homo sapi Aa154478 homo sapi Aa15447 homo sapi

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AAF66138

1D AAF66138

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1D CO-MAR-2004 (TEMBLEAL 27, Created)

1D CO-MAR-2004 (TEMBLEAL 27, Last sequence update)

1D CO-MAR-2004 (TEMBLEAL 27, Last sequence update)

1D CO-MAR-2004 (TEMBLEAL 27, Last annotation update)

1D CO-MAR-2004 (TEMBLEAL 27, Last annotation update)

1D URF4 GENE, PARTIAL COS; TRNA-HIS, TRNA-SER, AND

1D TRNA-LEU GENES, COMPLETE SEQUENCE; AND URF5 GENE, PARTIAL CDS;

1D MITOCHONDRIAL GENES FOR MITOCHONDRIAL PRODUCTS (Fragment).

1D MITOCHOMOTION.

2D MITOCHOMOTION.

3D MITOCHOMOTION.

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NU4M HUMAN STANDARD; PRT; 459 AA.

D 1305 ; Q8HNR8; 101, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-1986 (Rel. 04, Last annotation update)
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BLDLINE-824242101; PubMed-6284948;
Brown W.B. P.C.;
Brown W., Prager E.M., Wang A., Wilson A.C.;
"Mitochondrial DNA sequences of primates: Tempo and mode of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 76; DB 2; Length 152;
Pred. No. 0.00011;
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                     Q9B2X8
Q9B2Y5
Q9B2Y7
Q9B30V
Q6WGY1
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AAL54419
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EMBL, L00016; AAF66138.1; -.
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NON_TER 152 AA, 16905 MW, 1
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Matches 14; Conservative
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NU4M_HUMAN
Q6RL39
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Maximum Match 100%
Listing first 45 summaries
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Q6VHV8
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
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SEQUENCE FROM N.A. MEDLINE=81173052; PubMed=7219534; Anderson S., Bankier A.T., Barrell B.G., de Bruijn M.H.L.

NCBI_TaxID=9606;

homo sapien homo sapien pan paniscu homo sapien homo sapien

Q9B187 Q9B2W2 Q9B2W5

Q9B0T8

29B188

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MEDLINE=22723755; PubMed=12840039; DOI=10.1101/gr.686603;
Ingman M., Gyllensten U.;
"Mitochondrial genome variation and evolutionary history of Australian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=14760490; DOI=10.1007/s00414-004-0427-6; Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T., Irwin J.A., Parsons T.J.; "Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians."; Int. J. Legal Med. 118:137-146(2004).
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                                                                                                                                                                                               MEDIINE=22315217; PubMed=1377597;

Lu X., Walker T., Macmanus J.P., Seligy V.L.;

"Differentiation of HT-29 human colonic adenocarcinoma cells

correlates with increased expression of mitochondrial RNA: effects of

trehalose on cell growth and maturation.";

Cancer Res. 52:3718-3725(1992).
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"Mitochondrial genome diversity of native Americans supports a single
early entry of founder populations into America.";
Am. J. Hum. Genet. 71:187-192(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed=12949126; DOI=10.1093/molbev/msg220;
Mollanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in segment of MTNDS gene in haplogroup J.";
Mol. Biol. Evol. 20:2132-2142(2003).
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Lezza A.M., Elsas L.J. II, Nikoskelainen E.K.,
"Mitochondrial DNA mutation associated with Leber's hereditary optic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Silva W.A. Jr., Bonatto S.L., Holanda A.J., Ribeiro-Dos-Santos A.K., Paixao B.M., Goldman G.H., Abe-Sandes K., Rodriguez-Delfin L., Barbosa M., Paco-Larson M.L., Petzl-Erler M.L., Valente V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21012010; PubMed=11130070; DOI=10.1038/35047064; Ingman M., Kaessmann H., Paabo S., Gyllensten U.; "Mitochondrial genome variation and the origin of modern humans."; Nature 408:708-713(2000).
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"Mitochondrial DNA sequences of primates: tempo and mode of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A., AND VARIANT PRO-79.
MEDLINE=22062553; PubMed=12022039;
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Science 242:1427-1430(1988)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Bolhuis P.A., van Oost B.A.,
"Genetic and biochemical impairment of mitochondrial complex I
activity in a family with Leber hereditary optic neuropathy and
                                                                   "Electron transfer properties of NADH:ubiquinone reductase in the NDI/3460 and the ND4/11778 mutations of the Leber hereditary optic neuroretinopathy (LHON).";
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            CHARACTERIZATION OF VARIANT LHON HIS-340.
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                                                                                                                    FEBS Lett. 292:289-292(1991).
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SEQUENCE FROM N.A.

PubMed=14766490;

PubMed=14766490;

Irohle M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

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"Single nucleotide polymorphisms over the entire mtDNA genome that
increase the power of forensic testing in Caucasians.";

Int. J. Legal Med. 0:0-0(2004).

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Mitochondrion.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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87.5%; Pred. No. 0.00036;
live 1; Mismatches 1; Indels
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RMED, A4495147, AA693246.1, -.

GO, GO:0005739; C:mitochondrion; IEA.

RILEEPEO; IPR00318; NADHIMD oxred4.

RILEEPEO; IPR0010227; NDH IM.

RILEEPEO; IPR001750; Oxidored_q1.

RILEEPEO; IPR00150; Oxidored_q2.

RILEEPEO; IPR01039; Oxidored_q5.N.

Pfam; PF00159; Oxidored_q5.N.

REAM; PF00159; Oxidored_q5.N.

REAM; PF01059; Oxidored_q5.N.

RICRPAMA; TIGR01972; NDH IM.

RICRPAMA; TIGR01975; NDH IM.

SEQUENCE 459 AA; 51546 MW; FCECFC59DBD6971A CRC64;
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89.4%; Score 76; DB 2; Length 455
Best Local Similarity 87.5%; Pred. No. 0.00036;
Matches 14; Conservative 1; Mismatches 1; Indels
InterPro; IPR003918; NADHub oxred4.
InterPro; IPR001227; NDH I M.
InterPro; IPR001750; Oxidored q1.
InterPro; IPR00150; Oxidored q2.
InterPro; IPR00260; Oxidored q1.
InterPro; IPR00561; Oxidored q1, I.
Ffam; PF00159; Oxidored q1, I.
PRINTS; PR01437; NUOXDRDTASE4.
ITGREAMs; TIGR01972; NDH I M; NICCHONGION; NAD; Oxidored q1.
Mitochondrion; NAD; Oxidored q1.
Mitochondrion; NAD; Oxidored q1.
SEQUENCE 459 AA; 51568 MW; 864A4A13C81244C7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGRQN9 PRELIMINARY, PRT, 459 AA. GGRQN9; CJUL-2004 (TrEMBLrel. 27, Created) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
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Q6VHV8;
O5-JUL-2004 (TrEMBLrel. 27, Created)
O5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 4.
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Best Local Similarity 87.5'
Matches 14; Conservative
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Irwin J.A., Parsons T.J.;
"Single nucleotide polymorphisms over the entire mtDNA genome that increase the power of forensic testing in Caucasians.";
Int. J. Legal Med. 0:0-0(2004).
Int. J. Legal Med. O:0-0(2004).
EMBL; AR4D5316; ARMS9443.1;
GO:0005739; C:mitochondrion; IBA.
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Mitochondrion.
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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QGRL39;
QG-JUL-2004 (TrEMBLrel. 27, Created)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
OS-JUL-2004 (TrEMBLrel. 27, Last sequence update)
NADH dehydrogenase subunit 4.
  or send an email to license@isb-sib.ch)
                                                                            AY495091, AAR92501,
AY495091, AAR925501,
AY495093, AAR92542,11,
AY495094, AAR92555,11,
AY495094, AAR92558,11,
AY495097, AAR92588,11,
AY495097, AAR92581,11,
AY495099, AAR92607,11,
AY495100, AAR926201,
AY495101, AAR92646,11,
AY495101, AAR92659,11,
AY495101, AAR92669,11,
AY495101, AAR92669,11,
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PubMed=14760490;
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EMBL, AY495098;
EMBL; AY495099;
EMBL; AY495100;
EMBL; AY495101;
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EMBL; AY495103;
EMBL; AY495104;
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Name=ND4;
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PROUBLICE FROM N.A.

PubMeda14766490;

RA Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

RA Coble M.D., Just R.S., O'Callaghan J.E., Letmanyi I.H., Peterson C.T.,

RA Train J.A., Parsons T.J.;

RT "fingle nuclectide polymorphisms over the entire mtDNA genome that

Intrase the power of forensic testing in Caucasians.";

RIL INT. J. Legal Med. 0:0-0(2004).

C. -! CATALYITY AAP91151.]

DR EMBL; AV339564; AAP91164:1; -.

DR EMBL; AV339563; AAP91164:1; -.

DR EMBL; AV339563; AAP91138:1; -.

DR EMBL; AV339563; AAP91138:1; -.

DR EMBL; AV339563; AAP91138:1; -.

DR InterPro; IPRO102919; NabDub oxred4.

DR InterPro; IPRO10290; Oxidored_q1.

INTERPRO; IPRO1059; Oxidored_q1.

DR Ffam; PPO1059; Oxidored_q5 N; 1.

DR Pfam; PPO1059; Oxidored_q5 N; 1.

DR PRINTS; PRO1437; NUCXDRDTASG4.

KW Mitcochodarion; NAD; Oxidoredqtase; Ubiquinone.

SQUENCE 459 AA; 51564 WW; 55C25A6667D275BA CRC64;
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                                                                                                                                                                                                 PubMed=12949126;
Mollanen J.S., Finnila S., Majamaa K.;
"Lineage-specific selection in human mtDNA: lack of polymorphisms in a segment of MIND5 gene in happlogroup J.";
Mol. Biol. Evol. 20:2132-2142(2003).
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Mitochondriton.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
            Homo sapiens (Human).
Mitochondrion.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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05VI80; (TEMBLrel. 27, Created)
05-JUL-2004 (TEMBLrel. 27, Last sequence update)
05-JUL-2004 (TEMBLrel. 27, Last annotation update)
                                                                                              SEQUENCE FROM N.A.
MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonen M.S., Majamaa K.;
Finnila S., Lehtonen M.S., Majamaa K.;
Finnila S., Humcheneric network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484 (2001).
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MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonen M.S., Majamaa K.;
"Phylogenetic network for European mEDNA.";
Am. J. Hum. Genet. 68:1475-1484(2001).
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                                                                   NCBI_TaxID=9606;
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RP SEQUENCE FROM N.A.

RA PubMed=12949126;

RA Moilanen J.S., Finnila S., Majamaa K.;

RT "Lineage-specific selection in human mtDNA: lack of polymorphisms in a segment of MTNDS gene in haplogroup J.";

RL MOIL Biol. Evol. 20:2132-2142(2003).

CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

DR EMBL; AY339551; AAP910095.1; -.

DR EMBL; AY339551; AAP910081; -.

DR EMBL; AY339551; AAP910081; -.

DR GO, GO:0005739; C:mitochondrion; IEA.

DR InterPro; IPR001379; NADHULD oxred4.

DR InterPro; IPR001750; Oxidored_q1.

DR Pfam; PF00165; Oxidored_q1.

DR Pfam; PF00169; Oxidored_q1.

DR Pfam; PF00169; Oxidored_q5.N; 1.

DR Pfam; PF00197; NUOXDRDFASE4.

DR PTGRFAMS; TIGR01975, NDH I M. I.

RM Mitochondrion; NAD; Oxidoreductase; Ubiquinone.

SQUENCE 459 AA; 51656 MW; 2005581F3BD270AF CRC64;

SEQUENCE 459 AA; 51656 MW; 2005581F3BD270AF.
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SEQUENCE FROM N.A.

PubMed=1249126;

Moilanen U.S., Finila.S., Majamaa K.;

Segment of MINIDS gene in haplogroup J.";

Moilanen C. Majasa M. Musasa M. Majasa M. Musasa M. Majasa M.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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Pred. No. 0.00036;
1; Mismatches 1; Indels
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MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonen M.S., Majamaa K.;
Finnila S., Lehtonen M.S., Majamaa K.;
Filnila S., Lehtonen M.S., Majamaa K.;
Am. J. Hum. Genet. 68:1475-1484 (2001).
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05-JUL-2004 (TrEMBLrel. 27, Created)
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hes 14; Conservative
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Mitochondrion.
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Query Match

QEVLUS;

Q6VLUS

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MEDLINE=22723755; PubMed=12840039;
Ingman M., Gyllensten U.;
Mitochondrial genome variation and evolutionary history of Australian and New Guinean aborigines.";
Genome Res. 13:1600-1606(2003).
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
EMBL; AY289064; AAP48058.1; --
GO; GO:0005739; C:mitochondrinon; IEA.
GO; GO:0005739; C:mitochondrinon; CO; GO:0016491; F:OXAGORG eductase activity; IEA.
GO; GO:0016491; F:OXAGORG eductase activity; IEA.
GO; GO:0016491; F:OXAGORG eductase activity; IEA.
GO; GO:0016491; P:OXAGORG eductase activity; IEA.
GO; GO:0016491; P:OXAGORG eductase activity; IEA.
GO; GO:0016491; P:Mitochondrial electron transport; IEA.
                                                                                                                        Cabrera V.M.; "Mitochondrial DNA transit between West Asia and North Africa inferred
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I from U6 phylogeography.

I caralytic Activity: NaDH + ubiquinone = NAD(+) + ubiquinol.

I caralytic Activity: NaDH + ubiquinone = NAD(+) + ubiquinol.

R EMBL; AY275537; AAQ19456.1; -

R GO; GO:0005739; C:mitochondrion; IEA.

R InterPro; IPR001227; NADH I M.

InterPro; IPR001227; NADH I M.

R InterPro; IPR001227; NADH I M.

R InterPro; IPR001250; Oxidored q1.

R Pfam; PF00361; Oxidored q1. 1.

R Pfam; PF00361; Oxidored q1. 1.

R Pfam; PF001437; NADEDTASS4.

R RIGRAMS; TIGR01922; NAH I M.

Mitochondrion; NAD; Oxidoredutase; Ubiquinone.
[1]
ERUJENCE FROM N.A.
Pubbled=14563219;
Maca-Meyer N., Gonzalez A.M., Pestano J., Flores C., Larruga J.M.,
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Pred. No. 0.00036;
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InterPro; IPR010227; NDH I M.
InterPro; IPR010227; NDH I M.
InterPro; IPR001260; Oxidored q1.
Fram; Pr01061; Oxidored q1, 1.
Pfam; Pr01069; Oxidored q5, N; 1.
Pfam; Pr01069; Oxidored q5, N; 1.
Mitochondrio; Nab; Oxidoreductase; Ubiquinone.
SEQUENCE 459 AA; 51667 MW; 645F21839F906A55 CRC64;
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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ilarity 87.5%; Pred. No. 0.00036;
Conservative 1; Mismatches 1;
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Name=ND4;
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Best Local Similarity 8/...
Thes 14; Conservative
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Best Local Similarity
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Q7Y7B0;
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Q7Y7B0
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SECURACE FROM N.A.

Moilanen J.S., Finnila S., Majamaa K.;

T. Lineage-specific selection in human mtDNA: lack of polymorphisms in a segment of MYNDS gene in haplogroup J.";

Moil Biol. Evol. 20:2132-2142 (2003)

T. L. CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

REMBL; AV334044; AAP890711 j. .

REMBL; AV334044; AAP890711 j. .

ROJ GO:0005739; C:mitochondrion; IEA.

InterPro; IPR001227; NDH I.M.

InterPro; IPR001750; Oxidored q1.

InterPro; IPR001750; Oxidored q2.

Rem; PP001053; Oxidored q5.N.

Pfam; PP01053; Oxidored q5.N.

PRINTS; PR01437; NUOXDRDIASE4.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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89.4%; Score 76; DB 2; Length 459; 87.5%; Pred. No. 0.00036; 1; Mismatches 1; Indels
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87.5%; Pred. No. 0.00036;
Live 1; Mismatches 1; Indels
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Itochondrion; NAD; Oxidoreductase; Ubiquinone.
SQUENCE 459 AA; 51652 MW; 2EEE581C5BD270AF CRC64;
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05-JUL_2004 (TrEMBLrel. 27, Last sequence update)
05-JUL_2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 4.
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MEDLINE=21313109; PubMed=11349229;
Finnila S., Lehtonen M.S., Majamaa K.;
Phylogenetic network for European mtDNA.";
Am. J. Hum. Genet. 68:1475-1484(2001).
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Matches 14; Conservative
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Mitochondrion.
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Mitochondrion.
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SEQUENCE FROM N.A.
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Q7YCD8
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EMBL; AV289072; AAP48162.1; -.

GO; GO:0005739; C:nitocondarion; IEA.

GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

GO; GO:0008137; F:NADH dehydrogenase activity; IEA.

GO; GO:0006120; P:ATP synthesis coupled electron transport; IEA.

GO; GO:0006120; P:Mitochondrial electron transport, NADH to u. .; IEA.

InterPro; IPR010227; NDH I.M.

InterPro; IPR000156; Oxidored q1.

InterPro; IPR000560; Oxidored q5.N.

Ffam; PF01059; Oxidored q5.N.

TIGRPAMS; TIGR01972; NDH I.M.;

Mitochondrion; NAD; Oxidored q5.N; 1.

Mitochondrion; NAD; Oxidored q1. M; 34DD711F3BC3915F CRC64;
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-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
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Kong Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhu C.-L., Zhang Y.-P.;
"Phylogeny of East Asian Mitochondrial DNA Lineages Inferred from
Am. J. Hum. Genet. 0:0-0(2003).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 4.
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
NADH dehydrogenase subunit 4.
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87.5%; Pred. No. 0.00036;
tive 1; Mismatches 1;
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                                            417 GSLTHHINNMKPSFTR 432
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Complete Sequences.,

Am. J. Hun. Genet. 0:0-(0.2003).

-!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

EMBL, AY255163; AA067017.1; -.

EMBL, AY255163; AA067017.1; -.

GO; GO:0008137; F:NADH dehydrogenes (ubiquinone) activity; IEA.

GO; GO:0008137; F:NADH dehydrogenes activity; IEA.

GO; GO:0006120; P:NTP synthesis coupled electron transport; IEA.

GO; GO:0006120; P:mitochondrial electron transport, NADH to u. .; IEA.

InterPro; IPR010227; NDH I M.

InterPro; IPR010150; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GO; GO:0005739; C:mitochondrion; IEA.
GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
GO; GO:0016491; F:Oxidoreductase activity; IEA.
GO; GO:0016491; P:Oxidoreductase activity; IEA.
GO; GO:0016773; P:ATP synthesis coupled electron transport; IEA.
GO; GO:0006120; P:mitochondrial electron transport, NADH to u. . ; IEA.
MEDLINE=22723755; PubMed=12840039; Ingman M., Gyllensten U.; Mitcohndrial genome variation and evolutionary history of Australian and New Guinean aborigines."; Genome Res. 13:1600-1606(2003).
                                                                                                                                                                SEQUENCE FROM N.A. Kong Q.-P., Yao Y.-G., Sun C., Bandelt H.-J., Zhu C.-L., Zhang Y.-P., "Phylogeny of East Asian Mitochondrial DNA Lineages Inferred from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Mammalia, Eutheria, Primates, Catarrinii, Hominidae, Homo.
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InterPro; IPR01150; Oxidored q1.
InterPro; IPR00150; Oxidored q1.
InterPro; IPR00150; Oxidored q1.
Pfam; PF01059; Oxidored q5_N; 1.
Pfam; PF01059; Oxidored q5_N; 1.
TIGRPAMs; TIGR01972; NDH I.M.; 1.
SEQUENCE 459 AA; 51608 MW; 02E1F27CCF797BF5 CRC64;
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Mitochondrion.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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87.5%; Pred. No. 0.00036;
live 1; Mismatches 1; Indels
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InterPro, IPR000260, Oxidored_q5_N.

Pfam; PF00361; Oxidored_q1; 1.

Pfam; PF01059; Oxidored_q5_N; 1.

TIGRPAMS, TIGN-01972; NNF_I=M; 1.

Mitochondrion; NAD; Oxidoreductase; Ubiquinone.

SEQUENCE 459 AA; 51606 MW; 564652E26FC7851B CRC64;
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Q7YCF7;
Q7YCF7;
Q1-CCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NADH dehydrogenase subunit 4.
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1-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
NADH dehydrogenase subunit 4.
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Pred. No. 0.00036;
1; Mismatches 1;
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Mitochondrion.
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OC Nammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NX NCEI. TaxID=9666;

RP SEQUENCE FROM N.A.

RX MEDLINE=22723755; PubMed=12840039;

RA Ingman M., Gyllensten U;

RT "Michochondrial genome variation and evolutionary history of Australian

RT and New Guinean aborigines.";

RL Genome Res. 13:1600-1606(2003).

CC -!-CATALYTICA CATIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.

DR GO; GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.

DR GO; GO:0008137; P:NATP synthesis coupled electron transport; IEA.

DR GO; GO:0008137; P:NATP synthesis coupled electron transport; IEA.

DR GO; GO:0008137; P:NATP synthesis coupled electron transport; IEA.

DR InterPro; IPR001762; NDH I.M.

DR InterPro; IPR001762; Oxidored_q1.

DR Pfam; PF00159; Oxidored_q2.

DR Pfam; PF00159; Oxidored_q2.

DR TIORRAMS; TIGR01972; NDH I.M.

MICChondrion; NAD; Oxidored_q5.N.

MICChondrion; NAD; Oxidored_q5.N.

Altochondrion; NAD; Oxidored_q5.N.

Matches 14; Conservative 1; Mismatches 1; Indels 0; Gaps

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Search completed: November 10, 2004, 15:53:33

Job time: 27.8954 secs
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GenCore version 5.1.6

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OM protein - protein search, using sw model

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Sequence:
1 VSCWPSYLKYPLSTASASLLATQLKSIA 28
Scoring table: BLOSUM62
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Searched:
7 748139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139
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Pred. No. is the number of results predicted by chance to have

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ALIGNMENTS

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| Sequence 32717, Application US/09252991A | Sequence 32717, Application US/09252991A | Sequence 32717, Application US/09252991A | Sequence 32717, Application US/09252991A | Sequence 32717, Application US/09252991A | Sequence SELATING TO PERDOMONAS | TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS | TITLE OF INVENTION: NUMBER: US/09/252,991A | TITLE OF INVENTION: NUMBER: US/09/252,991A | CURRENT FILING DATE: 1999-02-18 | PRIOR APPLICATION NUMBER: US 60/074,788 | PRIOR APPLICATION NUMBER: US 60/094,190 | PRIOR PILING DATE: 1998-02-18 | NUMBER OF SEQ ID NOS: 33142 | SEQ ID NO 32717 | LENGTH: 372
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APPLICANT: JOHN N. SIMONS
APPLICANT: GENGE J. DAWSON
APPLICANT: GENGE G. SCHLAUDER
APPLICANT: GENGE G. SCHLAUDER
APPLICANT: THOMAS P. LEARY
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUBRHOFF
APPLICANT: ANTHONY SCOTT MUBRHOFF
APPLICANT: SHERI L. BUIJAK
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APPLICANT: SHERI L. BUIJAK
APPLICANT: SHERI L. BUIJAK
APPLICANT: SHERI L. SHIJAK
APPLICANT: SHERI NON-A, NON-B. NON-C, NON-D, NON-B. HEFATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 VSCWPS-----YLKYPLSTASASLLATQLKS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
34.4%; Score 48.5; D
Best Local Similarity 34.3%; Pred. No. 17;
Matches 12; Conservative 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 2
2.08-469-260A<sub>7</sub>214
; Sequence 214, Application US/08469260A
; Patent No. 6451578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-252-991A-32717
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PPDLCALLON
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMBKIT, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REPERRICE/DOCKET NUMBER: 5527.PC.01
TELEPRA: 708-937-63.65
; TELEPRA: 708-937-63.65
; INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
"TIME OF TELEPRA: TO BE TELEPRA:
          US/08/488,446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-214
          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  엄
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: JOHN N. SIMONS
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLANDER
APPLICANT: THOMAS P. LEARY
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: SHERI L. BUIJK
APPLICANT: 1SA K. MUSHAHWAR
ITILE OF INVENTION: NON-A, NON-B. NON-C, NON-C HEPATITIS
ITILE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABOTT
STREFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%; Score 48; DB 4; Length 50; 40.0%; Pred. No. 1.7; tive 4; Mismatches 11; Indels
                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SSEE: ABBOTT LABORATORIES D377/AP6D
F: 100 ABBOTT PARK ROAD
ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: ABBOTT LABORATORIES D377/AP6D STREET: 100 ABBOTT PARK ROAD CITY: ABBOTT PARK STATE STATE STATE STATE USA CUUNTRY: USA ZIP: 60064-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 WPSYLKYPLSTASASLLATQLKSIA 28
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Best Local Similarity 40.0%
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-469-260A-214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
TOPOLOGY: linear
             ADDRESSEE:
STREET: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-488-446-214
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RESULT 4

US-08-46-344A-214

Sequence 214, Application US/08467344A

Patent No. 6586568

EENERAL INFORMATION:

APPLICANT: JOHN N. SIMONS

GENCRGE J. DAMSON

GENCRGE G. SCHLAUDER

SURESH M. DESAI

THOMAS P. LEBRY

ANTHONY SCOTT MURRHOFF

JAMES C. ERKER

SEREEL L. BUIJOK

SURBELL L. BUIJOK

SURBELL L. BUIJOK

SURBELL L. BUIJOK

SURBELL N. SULOK

SURBELL N. SULOK

SURBELL N. SULOK

SURSHAWAR

TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS

REAGENTS AND METHODS FOR THEIR USE
                                                                                                                      Gaps
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CORRESPONDENCE ADDRESS:
ADDRESSE: ABBOTT LABORATCRIES D377/AP6D
STREET: 100 ABBOTT LABORATCRIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
CITY: ABBOTT PARK ROAD
CITY: BEDTT PARK
STATE: 100
COMPUTE: 105
COMPUTER: 107
COMPUTE
Query Match 34.0%; Score 48; DB 4; Length 50; Best Local Similarity 40.0%; Pred. No. 1.7; Matches 10; Conservative 4; Mismatches 11; Indels
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ATTORNEY/AGENT INFORMATION:
NAME: POREMESKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                 4 WPSYLKYPLSTASASLLATQLKSIA 28
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9 WPALVSTPLCTSEAKKLIFQLVTCA 33

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us-10-092-750-71.rai
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Sequence 214, Application US/08424550B

Patent No. 6720166

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: THOMAS P. LEARY
APPLICANT: SURESH M. DESAI
APPLICANT: SURESH M. DESAI
APPLICANT: SHERI L. BUIJK
APPLICANT: SHERI L. BUINK
APPLICANT
APP
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                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 50;
1.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11; Indels
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COUNTRY: USA
ZIP: 60064-3500
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENOTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 214:
                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
34.0%; Score 48;
Best Local Similarity 40.0%; Pred. No.
Matches 10; Conservative 4; Mismatc
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ATTORNEY/AGENT INFORMATION:
NAME: POFREMEKT, PRESCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
INPORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                  US-08-467-344A-214
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34.0%; Score 48; DB 3; Length 1244; 45.5%; Pred. No. 90;
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; Patent No. 6576442
; GENERAL INFORMATION:
; APPLICANT: Lev, Sima
; Plowman, Gregory D.
; Schlessinger, Joseph
; TILE OF INVENTION: RDGB PROTEINS AND RELATED
;
RESULT 6
US-08-938-291A-5
; Sequence 5, Application US/08938291A
; Patent No. 6117673
; GENERAL INFORMATION:
; APPLICANT: Lev, Sima APPLICANT: Plowman, Gregory D.
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
; TITLE OF INVENTION: PRODUCTS AND METHODS
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
COUNTRY: U.S.A.
ZIP: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 35 "Diskette, 1.44 MD
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COMPUTER: BM Compatible
COMPARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,291A
FILING DATE: September 26, 1997
CLASSIFICATION: 435
FILING DATE: October 11, 1996
ATTONNEY, AGBYT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
RELECHOMENICATION INFORMATION:
TELEFAX: (213) 489-1600
TELER: 67-5510
TELER: 67-5510
TELER: 67-5510
TELER: 67-5510
TELENGTH: 1244 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 PSYLKYPLSTASASLLATOLKS 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 45.5
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide US-08-938-291A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-589-619-5
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4 WPSYLKYPLSTASASLLATQLKSIA 28

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Fri Nov 12 14:56:00 2004

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ASOURT Sequence 18300, Application US/09252991A

Sequence 18300, Application US/09252991A

Sequence 18300, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION:

NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION:

TITLE OF INVENTION:

APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-02-18

NUMBER OF SEQ ID NOS: 33142

LENGTH: 235
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                                 Gaps
                                 8;
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                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5; Indels
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Sequence 2, Application US/09032372;
Patent No. 6008337;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Gueley, Neil C.
APPLICANT: Gueley, Neil C.
APPLICANT: Lal, Preet,
TITLE OF INVENTION: CELL CYCLE RELATED PROTEINS
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
STREET: 3174 Porter Drive
CETY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FEASESQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/032,372
FILING DATE: Herewith
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                           Query Match 32.6%; Score 46; DB Best Local Similarity 47.1%; Pred. No. 24; Matches 8; Conservative 4; Mismatches
       Best Local Similarity 40.0%; Pred. No. 29; Matches 12; Conservative 3; Mismatches
                                                                               ----STASASLLATOL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 SCWPSYLKYPLSTASAS 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 AAWPSWTPSPASTANAT 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           USA
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| Sequence 21362, Application US/09252991A
| Sequence 21362, Application US/09252991A
| Patent No. 6551795
| GENERAL INFORMATION:
| APPLICANT: Marc J. Rubenfield et al.
| TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
| TITLE OF INVENTION: AERCGIONAS FOR DIAGNOSTICS AND THERAPEUTICS
| TITLE OF INVENTION: AERCGIONAS FOR DIAGNOSTICS AND THERAPEUTICS
| CURRENT APPLICATION NUMBER: US/09/252,991A
| CURRENT FILING DATE: 1999-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-02-18
| PRIOR FILING DATE: 1998-07-27
| NUMBER OF SEQ ID NOS: 33142
| SEQ ID NO 21362
| LENGTH: 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
34.0%; Score 48; DB 4; Length 1244;
Best Local Similarity 45.5%; Pred. No. 90;
Matches 10; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%; Score 47; DB 4; Length 368;
CORRESPONDENCE ADDRESS:
ADDRESSEB: Lyon & Lyon
STREET: 633 West Fifth Street
SINTEE 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFFWARE: FeatSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,619
FILING DATE: 07-Jun-200
PRIOR APPLICATION AUMBER: US/08/938,291
FILING DATE: September 26, 1997
APPLICATION NUMBER: 06/027,337
FILING DATE: September 26, 1997
APPLICATION NUMBER: 1996
ATTORNEY/AGENT INFORMATION:
NAME: WAEDDLEY, RICCABART J.
REFERENCE/DOCKET NUMBER: 32,327
TELEPRONE/DOCKET NUMBER: 32,327
TELEPRONE; (213) 955-0440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-589-619-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 PSYLKYPLSTASASLLATQLKS 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1244 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
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à g Query Match

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NS-09-252-991A-23804

) Sequence 23804, Application US/09252991A

) Sequence 23804, Application US/09252991A

) Patent No. 6551703.

) GRNERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

APPLICANT: Marc J. Rubenfield et al.

) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

) TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

) TITLE OF INVENTION: ABOUT 1995-02-18

CURRENT RAPLICATION NUMBER: US 60/074,788

) PRIOR APPLICATION NUMBER: US 60/094,190

) PRIOR APPLICATION NUMBER: US 60/094,190

) PRIOR FILING DATE: 1998-02-18

) PRIOR FILING DATE: 1998-07-27

) NUMBER OF SEQ ID NOS: 33142

) LENGTH: 594
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Pred. No. 75;
2; Mismatches 10; Indels
                                                                                                                                         Query Match
32.6%; Score 46; DB 4; Length 438;
Best Local Similarity 33.3%; Pred. No. 52;
Matches 7; Conservative 9; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/08938291A
Fatent No. 6117673
GENERAL INFORMATION:
APPLICANT: Lev. Sina
APPLICANT: Plowman, Gregory D.
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
TITLE OF INVENTION: PRODUCTS AND METHODS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MD
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/938,291A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSER: Lyon & Lyon STREET: 633 West Fifth Street STREET: Suite 4700 CITY: Los Angeles STATE: California COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VSCWPSYLKYPLSTASASLLAT 22
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                                                                                                                                                                                                                                             1 VSCWPSYLKYPLSTASASLLA 21
                                                                                                                                                                                                                                                                         39 IARWPSPRRWPISSSSPAAMA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23804
                                                                         ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 32.6%;
Best Local Similarity 45.5%;
Matches 10; Conservative
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CURRENT APPLICATION DATA:
; SEQ ID NO 23034
; LENGTH: 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-938-291A-6
                                                     TYPE: PRT
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Betent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
FOR INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION:
FOR DIAGNOSTICS AND THERAPEUTICS
TOTHERY APPLICATION NUMBER:
US 60/074,725
PRIOR APPLICATION NUMBER:
US 60/096,409
PRIOR FILING DATE:
1998-02-13
PRIOR PILING DATE:
1998-03-13
PRIOR SEQ ID NOS:
28208
SEQ ID NO 21624
LENGTH: 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 23034, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO FSEUDOMONAS
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILLS OF INVENTION: AERGINOSA, POR DIAGNOSTICS AND THERAPEUTICS
FILLS OF INVENTION: AERGINOSA, POR DIAGNOSTICS AND THERAPEUTICS
FILLS REPERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-18
PRIOR PRILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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Pred. No. 48;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Score 46; DB 3;
Pred. No. 38;
2; Mismatches
     REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0478 US
TELECOMUNICATION INFORMATION:
TELEPHONE: 650-845-4166
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 PNYMPYPLSSEKSTLTPSEV 287
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Best Local Similarity 35.0%; Pro
Matches 7; Conservative 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               306 PDYLQYSISTALCSL 320
                                                                                                                                            INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 337 amino acids TYPE: amino acid strandedness: single TYPE: single TYPOLOGY: linear IMMEDIATE SOURCE: LIBRARY: UTRENOTO2 CLONE: 680517
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 32.6%;
Best Local Similarity 60.0%;
Matches 9; Conservative ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-21624
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US-09-248-796A-21624
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Gaps

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Query Match 32.6%; Score 46; DB 4; Length 1349; Best Local Similarity 40.9%; Pred. No. 2.1e+02; Matches 9; Conservative 5; Mismatches 8; Indels
             Search completed: November 10, 2004, 15:57:22 Job time : 12.9537 secs
                                                                                                                                                                                                                                                                                                                                                786 PRYQRYPLGDGCSTLLADVLQT 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lev, Sima
APPLICANT: Lev, Sima
Plowman, Gregory D.
Schlessinger, Joseph
TITLE OF INVENTION: RDGB PROTEINS AND RELATED
PRODUCTS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-206
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBW Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSeq
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/589,619
FILING DATE: O'Jun-2000
CLASSIFTCATION: AUKROWN>
PRION APPLICATION NUMBER: US/08/938,291
FILING DATE: September 26, 1997
APPLICATION NUMBER: US/08/938,291
FILING DATE: September 26, 1997
APPLICATION NUMBER: US/08/938,291
FILING DATE: OCTOBER 11, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REFERENCE/DOCKET NUMBER: 228/172
TELECOMMUNICATION INFORMATION:
TELEFAX: (213) 489-1600
TELEFAX: (213) 489-1600
FILING DATE: September 26, 199,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA: 60/027,337
FILING DATE: October 11, 1996
ATTORNEY/AGENT: INFORMATION:
NAME: Warburg, Richard J.
REGISTRAIDON NUMBER: 32,327
REGISTRAIDON NUMBER: 32,327
REJECHONE: (213) 489-1600
TELEFRAX: (213) 489-1600
TELEFRAX: (213) 489-1600
TELEFRAX: (213) 955-0440
TELERX: 67-310
INPORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
LENGTH: 1349 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           786 PRYORYPLGDGCSTLLADVLOT 807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-09-589-619-6
; Sequence 6, Application US/09589619
; Batent No. 6576442
; GENERAL INFORMATION:
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Sequence 214, App Sequence 174891, Sequence 145804, Sequence 177818, Sequence 200760, Sequence 200760, Sequence 201026, Sequence 201026, Sequence 201026, Sequence 122676, Apple Sequence 33, Appl Sequence 34, Appl Sequence 31069, Sequence 31069, Sequence 31069, Sequence 208, Appl Sequence 218, Appl Sequence 22, Appl Sequence 22, Appl Sequence 23, Appl Sequence 24, Appl

Scoring table:

Searched:

Minimum DB Maximum DB

Database

Perfect score:

Sequence:

OM protein

Run on:

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## Sequence 71, Application US/10092750

## Sequence 71, Application US/10092750

## Publication No. US20000032157A1

## GENERAL INFORMATION:

## APPLICANT: Hammond, Philip W.

## APPLICANT: Alphin, Julia

## APPLICANT: Aright, Martin C.

## TITLE OF INVENTION: Polypeptides Interactive with BCL-XI

## CURRENT PEPLICATION NUMBER: US/10/092,750

## CURRENT PEPLICATION NUMBER: US/0/202-03-07

## PRIOR FILING DATE: 2001-03-08

## NUMBER OF SEQ ID NOS: 253

## SOFTWARE: FastSEQ for Windows Version 4.0

## SEQ ID NO 71
     US-10-424-559-174891
US-10-427-963-174891
US-10-425-115-266647
US-10-425-115-266647
US-10-425-115-266647
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-201060
US-10-425-115-361069
US-10-408-765A-83
US-10-408-765A-83
US-10-408-765A-83
US-10-425-115-361069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 141; DB 14; Best Local Similarity 100.0%; Pred. No. 1.2e-13; Matches 28; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 VSCWPSYLKYPLSTASASLLATQLKSIA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VSCWPSYLKYPLSTASASLLATQLKSIA 28
TYPE: PRT
, ORGANISM: Homo sapiens
US-10-092-750-71
US-10-092-750-71
                                                                                      LENGTH: 28
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2435, Ap
163030,
167104,
2, Appli
143889,
4490, Ap
                                                                    November 11, 2004, 02:43:24; Search time 67.6584 Seconds (without alignments) 146.426 Million cell updates/sec
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Sequence
Sequence
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Sequence
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                                                                                                                                                                                                                                                                                            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-092-750-71
US-10-104-047-2435
US-10-424-599-167104
US-10-109-324-2
US-10-109-324-2
US-10-109-324-2
US-10-425-91-1490
US-10-425-91-3865
US-10-425-91-3565
US-10-437-963-132933
US-10-437-963-132933
US-10-437-963-132933
US-10-637-963-132933
US-10-637-963-132933
US-10-637-963-132933
US-10-637-963-132933
US-10-637-963-132933
US-10-637-963-13293
                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                        141
1 VSCWPSYLKYPLSTASASLLATQLKSIA 28
                                                                                                                                                                                   1568699 seqs, 353819137 residues
                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                 - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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928
149
173
1257
116
697
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176
113
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Match Length
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551
533
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Gaps

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Indels

RESULT 2
US-10-104-047-2435
Sequence 2435, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:

65245, A 132933, 279483, 304497,

Sequence Seq

49.5 49.5

Score

Length 28;

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Sequence 143889

is Sequence 143889

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| Sequence 2, Application No. US20030082682A1
| Publication No. US20030082682A1
| GENERAL INFORMATION:
| APPLICANT: Hinayana L. Bawagan
| APPLICANT: Kathryn B. Freeman
| APPLICANT: Kathryn B. Freeman
| APPLICANT: Atacong Li
| TITLE OF INVENTION: Polynuclectide and Polypeptide Sequence
| TITLE OF INVENTION: Polynuclectide and Polypeptide Sequence
| TITLE OF INVENTION: Of RXR Interacting Protein, RB204
| FILE REPERANCE: GPS0045
| FULR REPERANCE: GPS0045
| FURRENT PELLING DATE: 2002-03-28
| PRIOR APPLICATION NUMBER: 60/280,397
| PRIOR PELLING DATE: 2001-03-30
| NUMBER OF SEQ ID NOS: 2
| SOFTWARE: PastSEQ for Windows Version 4.0
| SEQ ID NO 2
| LENGTH: 1257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.6%; Score 53; DB 14; Length 1257; ilarity 40.0%; Pred. No. 93; Conservative 4; Mismatches 8; Indels (
                                                                                                                                                                                                                                                                                                     Score 53; DB 15; Length 173;
Pred. No. 10;
4; Mismatches 5; Indels
                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(173)
CTHER INFORMATION: unsure at all Xaa locations
FEATURE:
CTHER INFORMATION: Clone ID: PAT_MRT3847_121909C.1.pep
US-10-424-599-167104
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PEATURE:
OTHER OTHER ID: PAT_MRT3847_100945C.1.pep
US-10-424-599-143889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 SFLTRPLSTLSLSRLASQIES 107
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                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 57.1%;
Matches 12; Conservative
      TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: human
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US-10-109-324-2
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Publication No. US20040031072A1
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5,322)B
CURRENT APPLICANTON NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 167104
LENGTH: 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 163030, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
GENERAL INFORMATION
APPLICANT: La ROSa Thomas J
APPLICANT: La ROSa Thomas J
APPLICANT: La ROSa Thomas J
APPLICANT: Covalic David K
APPLICANT: Sover David K
APPLICANT: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 349
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39.0%; Score 55; DB 15; Length 349;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 11; Conservative 5; Mismatches 6; Indels
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20030236392Alel full length cDNA
FILE REFERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT FILING DATE: 2002-03-25
PRIOR PILING DATE:
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: Patentin Ver. 2.1
ERGTH 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_118233C.1.pep
US-10-424-599-163030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 IECWPSNSKYPLPVFSTFVL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSCWPSYLKYPLSTASASLL 20
                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
COGANISM: Homo sapiens
US-10-104-047-2435
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US-10-424-599-163030
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APPLICANT:
APPLICANT:
APPLICANT:
Boukharov, Andrey A.
APPLICANT:
Boukharov, Andrey A.
APPLICANT:
Boukharov, Andrey A.
APPLICANT:
Boukharov, Andrey A.
APPLICANT:
Li, Ping
TITLE OF INVENTION:
Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 132933
- FENGTH: 176
                      US-10-42-114-65245

Sequence 65245, Application US/10425114

Sequence 65245, Application US/10425114

Sequence 65245, Application No. US2004003488A1

Publication No. US2004003488A1

APPLICANT: Liu, Jingdong

APPLICANT: ADAU, Yinua

APPLICANT: APPLICANT: About K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE REFERENCE: 38-21(53313)B

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 73128

SEQ ID NO 65245

LENGTH: 715
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US-10-437-963-132933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; CTHER INFORMATION: Clone ID: LIB4745-009-A8_FLI.pep
US-10-425-114-65245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 132933, Application US/10437963; Publication No. US20040123343A1; GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Pay Wei
APPLICANT: Poukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brabazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S PSYLKYPLSTASAS -- LLATQLKSIA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                36 PSYLAYPICTDARAPVILNTTLKFCA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-10-424-599-279483
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Sequence 332665, Application US/10425115

Sequence 332665, Application US/10425115

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Las Rosa, Thomas J.
APPLICANT: Las Rosa, Thomas J.
APPLICANT: Las Los Invertions Usina K.
APPLICANT: Character Control of Control
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1 LOCATION: (72)
2 OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-08-764-891-4490
                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                          Sequence 4430, Application US/09764891
Fublication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT Rosen et al.
TITLE OF INVENTION: NUMBER: US/09/764,891
CURRENT APPLICANTION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper; NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4490
LENGTH: 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17; Length 697,
       DB 15; Length 56;
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                                                                      9; Indels
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US-10-425-115-332665
Query Match
36.9%; Score 52; DB:
Best Local Similarity 46.2%; Pred. No. 4.3;
Matches 12; Conservative 5; Mismatches
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36.2%; Score 51; DB
Best Local Similarity 53.8%; Pred. No. 96;
Matches 14; Conservative 2; Mismatches
                                                                                                                                                                                    25 SSTPSFIKTPLASFALSLTOTOLYHI 50
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                                                                                                                                        2 SCWPSYLKYPLSTASASLLATQLKSI 27
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-425-115-332665
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Gaps
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APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: ANTHONY SCOTT MUERHOFF
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAHWAR
TITLE OF INVENTION: NON-A, NON-B. NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
TOWNERS FOR SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
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                                                                                                                                                                                      Length 113;
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Pred. No. 15;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                 Query Match 34.4%; Score 48.5; DB 15; Best Local Similarity 61.1%; Pred. No. 31; Matches 11; Conservative 2; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 WPSYLKYPLSTASASLLATQLKSIA 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOHN N. SIMONS
TAMI J. PILOT-NATIAS
GEORGE J. DAWSON
GEORGE G. SCHLAUDER
SURESH M. DESAI
THOMAS P. LEARY
ANTHONY SCOTT MUERHOFF
JAMES C. EKKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 214, Application US/08424550B Publication No. US20020119447A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: ABBOTT LABORATORIES
I: 100 ABBOTT PARK ROAD
ABBOTT PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: PORBINBSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
                                                                                                                                                                                                                                                                                      2 SCWPSYLKYP-LSTASAS 18
                                                                                                                                                                                                                                                                                                                                  75 SCWPSWSQTPDLSDPSAS 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 214: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.0%;
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
               SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3204
LENGTH: 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 50 amino acids amino acids
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                                                                                       TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                                                                        US-10-108-260A-3204
                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-424-550B-214
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; Sequence 304497, Application US/10425115
; Sequence 304497, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: La Rovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants
; TITLE REFERENCE: 38-21 (53222)
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 304497
Sequence 279483, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: La Rose Thomas J
APPLICANT: La Rose Thomas J
APPLICANT: Cao Vinua
APPLICANT: Cao Vinua
APPLICANT: Cao Vinua
APPLICANT: Cao Vinua
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILLS REPERENCE: 38 2213 B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 279483
LENGTH: 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Publication No. US20040005560A1
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Clone ID: PAT_MRT3847_94396C.1.pep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: MRT4577_40771C.1.pep
US-10-425-115-304497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
34.8%; Score 49; DB 17;
Best Local Similarity 40.9%; Pred. No. 19;
Matches 9; Conservative 3; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WPSYLKYPLSTAS-ASLLATOLK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 WPASLKYILSCVSVASILSPHLQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 WPSYLKYPLSTASASLLATQLK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 WPSWIDFPFSTVVERLYLLELK 82
                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-424-599-279483
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US-10-108-260A-3204
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US-10-424-59-174891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure

LOCATION: (1). (63)

OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
FRATURE:

OTHER INFORMATION: Clone ID: PAT_MRT3847_128946C.1.pep
US-10-424-599-174891
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5.1.6	Compugen Ltd.
rsion	- 2004
GenCore	(c) 1993 - :
	Copyright

OM protein - protein search, using sw model

Run on:

November 10, 2004, 14:52:32; Search time 9.56584 Seconds (without alignments) 281.634 Million cell updates/sec

US-10-092-750-71 141 1 VSCWPSYLKYPLSTASASLLATQLKSIA 28 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: * Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	e III sec	hypothetical prote	membrane-associate	hypothetical prote	ņ	conserved hypothet	hypothetical prote	beta-N-acetylgluco	dihydroaeruginoic	hypothetical prote	hypothetical trans	probable non-proce	ple	gene frizzled prot	hypothetical prote	ä	hypothetical prote	hypothetical prote	photosystem II oxy	photosystem II oxy	l prot	DNA gyrase chain B	polykeitde synthas	polyketide synthas	hypothetical prote	myosi	ical prc	related
SOUTHWALLES	A10033	9035	5	D72647	AD1824	A82449	T34438	107900	T17402	T47326	C95847	C97013	852677	503540	T43449	A44062	T29204	H70951	JC4015	T01747	D75317	T43906	C98275	AC3009	T32644	458	H85362	342
DB	2.2	1 74	7	7	7	7	7	~	N	N	N	N	N	N	(7	Н	N	N	~	N	N	N	0	ď	N	N	N	N
Length	306	137	1243	376	552	320	342	603	1438	112	286	425	507	581	877	3068	680	1055	213	217	250	388	491	491	494	1502	2895	208
% Query Match	36.2	4.	4.	33.7	ص	33.3	٠ ص	ë.	33.3	32.6	ά.	ď,	ď.	ď.	ď	ď	ď.	ά.	Η.	31.9	ή.	ä	31.9	ä	ä	31.9	ä	31.6
Score	51	48.5	48	7.	•	47	47	47	47	46	46	46	46	46	46	46		45.5	45	45	45	45	45	45		45	45	44.5
Result No.	:	ım	4	S	ø	7	ထ	σι	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

ribonuclease H rnh exodeoxyribonuclea	hypothetical prote	hypothetical prote	ribosomal protein	conserved hypothet	hypothetical prote	hypothetical prote	DNA gyrase chain B	conserved hypothet	dopamine receptor	R transactivator h	probable membrane	hypothetical prote	hypothetical prote	nonstructural poly	
C69693	T21283	T31478	R3EGS2	F82707	E71520	H64372	T43900	B69875	C55886	C45710	564539	T20544	AE2011	872349	
010	10	C)	н	(1	N	C3	(7	N	N	~	8	0	~	0	
255	1307	171	240	259	335	365	388	415	444	552	609	1187	1601	2493	
31.6	31.6	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	31.2	
44.5	44.5	44	44	44	44	44	44	44	44	44	44	44	44	44	
30	9 6	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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	RESULT 1	
	AlDUJ3 ALDUJ3 Type III secretion system apparatus protein [imported] - Yersinia pestis (strain C092)	0
	C'Species: Yersinia pestis	
-	C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004	
	C; Accession: AI0033	
	R; Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B	1.B
	deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;	
	il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,	ij,
	Nature 413, 523-527, 2001	
	A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.	
	A; Reference number: AB0001; MUID:21470413; PMID:11586360	
	A; Accession: A10033	
	A;Status: preliminary	
	A; Molecule type: DNA	
	A;Residues: 1-306 <kur></kur>	
	A; Cross-references: UNIPROT: Q8ZJ53; GB: AL590842; PIDN: CAC89132.1; PID: 915978370; GSPDB:	В:
_	C; Genetics:	
	A;Gene: YP00269	
	Query Match 36.2%; Score 51; DB 2; Length 306;	
_	Best Local Similarity 43.5%; Pred. No. 7.3;	
	Matches 10; Conservative 4; Mismatches 9; Indels 0; Gaps 0;	
	Qy 2 SCWPSYLKYPLSTASASILATQL 24	
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tyrs protein sirio33 - Synechocystis sp. (strain PCC 6803) C;Species: Synechocystis sp. C;Species: Synechocystis sp. C;Acriety: PCC 6803 C;Accession: 575255 C;Accession: 575255 S; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N. C,X.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud DNA Res. 3, 109-136, 1996 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocysti

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C;Accession: D72647
R;Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takakawa, H.; Zakamarabayasi, Y.; Jin-no, K.; Takakawa, H.; Zakamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; E DNA Res. 6, 83-101, 1999
A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropy; A;Reference number: A72450; MUID:99310339; PMID:10382966
A;Accession: D72647
A;Accession: D72647
A;Molecule type: DNA
                                                                                                                                                                                                                                                                     A, Residues: 1-376 <KAW>
A, Cross-references: UNIPROT: Q9YEG6, DDBJ: AP000060; NID: g5104188; PIDN: BAA79580.1; PID:d3
A, Experimental source: strain K1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: AD1824
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch;
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, E. A. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ans A;Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1-320 <HEI>
A;Cross-references: UNIPROT:Q9KW64; GB:AE004383; GB:AE003853; NID:g9657927; PIDN:AAF964;
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   periplasmic oligopeptide-binding protein of oligopeptide ABC transporter alr0140 [import C,Species: Nostoc sp. PCC 7120
A,Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein VCA0524 [imported] - Vibrio cholerae (strain N16961 sero
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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: Ag2449
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Arture 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 376;
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                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: APE0610
C;Superfamily: Aeropyrum pernix hypothetical protein APE0610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , Match
Local Similarity 37.0%; Pred. No. 30;
les 10; Conservative 7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 VSCWPSYLKYPLSTA---SASLLATOL 24
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Best Local Similarity 46.4%;
Matches 13; Conservative
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A,Status: preliminary
A,Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 preliminary
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Best Local S:
Matches 10
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C;Species: Mus musculus (house mouse)
C;Species: Mus musculus (house mouse)
C;Species: Og-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
C;Accession: JC5615
R;Aikava, Y; Haza, H; Watanabe, T.
B;Aikava, Y; Haza, H; Watanabe, T.
B;Aikava, Y; Haza, H; Watanabe, T.
B;Aichen: Biophys: Res. Commun. 336, 559-564, 1997
A;Title: Molecular cloning and characterization of mammalian homologues of the Drosophil A;Reference number: JC5615, MUID:97396134; PMID:9245688
A;Contents: Brain
A;Accession: JC5615
A;Status: nucleic acid sequence not shown
A;Residues: nucleic acid sequence not shown
A;Residues: 1-1243 cAIK>
A;Consentic type: mRNA
A;Residues: J-1243 cAIK>
A;Consent: This protein plays a role in brain development, at a particular stage by tran A;Gene: mpt-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: UNIPROT:097X41; GB:AE006641; NID:g13815181; PIDN:AAK42107.1; GSPDB:q
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chan-
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Rishe, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jorg, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jorg, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan Jorg, J.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, submitted to GenBank, April 2001
A.Description: Sulfolobus solfataricus complete genome.
A.Reference number: A99139
A.Reference number: A99139
A.Reference number: A99139
A.Residues: 1-137 <KUR>
A.Residues: 1-137 <KUR>
A.Residues: 1-137 <KUR>
A.Genetics:
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                                                                                                                                                                                                                                                                                                                           hypothetical protein SSO1914 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: S4-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004 C;Accession: D90356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 membrane-associated phosphatidyl inositol transfer protein - mouse C;Species: Mus musculus (house mouse)
C;Species: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
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C;Species: Aeropyrum pernix
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
                                                                  Gaps
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   Score 50; DB 2; Length 565;
Pred. No. 20;
7; Mismatches 9; Indels
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Pred. No. 7.3;
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Pred. No. 89;
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Matches 12; Conservative
      35.5%;
Similarity 36.0%;
9; Conservative
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llarity 45.5%;
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Matches 10; Conserv
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Best Local S
Matches 9
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dihydroaeruginoic acid synthetase (EC 6.3.2.-) - Pseudomonas aeruginosa Gispecies: Descrippinosa Gispecies: Descrippinosa Gispecies: I5-Oct-1999 #text_change 09-Uul-2004 Giaccession: T17402; D83118 Microbiology 144, 3135-3148, 1998 Microbiology 144, 3135-3148, 1988 Microbiology 144, 2000 Microbiology 2000 Microbiolo
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T47326
R;Monfort, A.; Casacuberta, E.; Puigdomenech, P.; Mewes, H.W.; Rudd, S.; Lemcke, K.; Ma submitted to the Protein Sequence Database, April 2000
A;Accession: T47326
A;Accession
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40.0%; Pred. No. 1.5e+02;
tive 3; Mismatches 7;
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58.8%; Pred. No. 14;
cive 3; Mismatches
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C;Function:
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A; Description: The sequence of C. elegans cosmid K11H12.
A; Reference number: 221526
A; Reference number: 123426
A; Accession: 134448
A; Residue: preliminary; translated from GB/EMBL/DDBJ
A; Residue: 1-342 - GRA>
A; Residues: 1-342 - GRA>
A; Residues: 1-342 - GRA>
A; Cross-references: UNIPROT: P91373; EMBL: U88168; PIDN: AAC24402.1; GSPDB: GN00022; CESP: K1, Cross-references: UNIPROT: P91373; EMBL: U88168; PIDN: AAC24402.1; GSPDB: GN00022; CESP: K1, A; Experimental source: strain Bristol N2; clone K11H12
A; Experimental source: strain Bristol N2; clone K11H12
A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Genet
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A,Residues: 1-603 «KIM»
A,Cross-references: UNIPROT:09HGI3; DDBJ:AB039846
C,Comment: This enzyme is generally dimeric and has broad substrate specificity. It has
gradation of chitin cell wall by endochitinases.
C,Genetics:
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JActe: 29-0ct.1999 #sequence_revision 29-0ct.1999 #text_change 09-Jul-2004
JAccession: T34438
Bradshaw, H.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein K11H12.8 - Caenorhabditis elegans
                                                                                                                                                                                                  core 47; DB 2;
red. No. 30;
Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 2;
Pred. No. 32;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           105 WPSYVRERISTTYAYLAGSLALTAVSGVA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 WPSYLKYPLSTASA----SLLATOLKSIA 28
                                                                                                                                                                                                       Score 47;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSYLKYPLSTASASLLATOLK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  134 PSWFLYPVGVISSSLAGTO 152
                                                                                                                                                                                                                                                                                           3;
                                                                                                                                                                                                                                                                                                                                                                                              5 PSYLKYPLSTASASLLATQ 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Gene: nagA
C,Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%;
                                                                                                                                                                                            33.3%;
ilarity 47.4%;
Conservative
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Matches 11; Conservative
                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 9; Conserv
C;Genetics:
A;Gene: VCA0524
A;Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        83
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Gene frizzled protein precursor - fruit fly (Drosophila melanogaster)
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Species: Drosophila melanogaster
C.Species: John 1990 #sequence travision 31-Mar-1990 #text_change 09-Jul-2004
C.Accession: 803540; 815708; 815708
Nature 318, 263-264, 1989
Nature 318, 263-264, 1989
A.Accession: 633-264, 1989
A.Accession: 803540; MUID:89159415; PMID:2493583
A.Accession: 803540; MUID:89159415; PMID:2493583
A.Molecule type: mRNA
A.Molecule type: mRNA
A.Molecule type: MRNA
A.Residues: 1-581 cVIN>
A.Conover, S.; Klein, L.
Genetics 126, 401-416, 1990
A.Atler 126, 401-416, 1990
A.Atler Molecular structure of frizzled, a Drosophila tissue polarity gene.
                                                                                                                                                                                                                                                                         Anches of the content C;Date: 19-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: S52677
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A)Molecule type: DNA
A)Molecule type: DNA
A)ACCESS-references: EMBL:X54648; NID:g7973; PIDN:CAA38460.1; PID:g804979
A)ACCESSION: S15709
A)Status: preliminary
A)Molecule type: DNA
A)Residues: 1-405, WX', 408, WQFHTIN' <AD2>
A)Cross-references: EMBL:X54648; NID:g7973; PIDN:CAA38461.1; PID:g804980
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A;Introns: 224/3; 264/3; 329/3; 405/1
C;Superfamily: fruit fly frizzled protein
C;Keywords: alternative splicing; transmembrane protein
F;1-26/Domain: signal sequence #status predicted <SIG>F;27-581/Product: gene frizzled protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.6%; Score 46; DB 2; Length 507; 62.5%; Pred. No. 69; tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.6%; Score 46; DB 2; Length 581; 33.3%; Pred. No. 79; ive 6; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              145 WPENLECSKFPVHGGEDLCVAENTTSSASTAATPTRSVA 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---STASASLLATQLKSIA 28
                                                                                                                                                 March 1995
                                                                                R;Murphy, L.; Shore, L.; Harris, D. submitted to the EMBL Data Library, A;Reference number: $52671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             198 QYPLYTASASLFNAQV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 KYPLSTASASLLATOL 24
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nes 13; Conservative
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Matches 10, Conservative
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Best Local S:
Matches 13,
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                                                                                                                                                                               C;Species: Sinorhizobium melilot: C;Species: C;Sp
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J. Bally, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Batcheriol. 181, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clc A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: C97013
A;Sterium Clc A;Residues: L925 cKUR>
A;Residues: 1-425 cKUR>
A;Residues: 1-425 cKUR>
A;Cross-references: UNIPROT:Q97KK1; GB:AE001437; PIDN:AAK78894.1; PID:g15023818; GSPDB:GC;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable non-processive endoglucanase family 5, ortholog of mannase A, secreted, dockeri
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: C97013
R;Nolling, J.; Breton, G.; Omelchenko. M V. Narbranne.
                                                                                                                                                 protein SMb20040 [imported] - Sinorhizobium meliloti (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32.6%; Score 46; DB 2; Length 425; 52.6%; Pred. No. 57; tive 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 VICWALVLSLPVMT--ALMLATMPSSLA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 VSCWPSYLKYPLSTASASLLATOLKSIA 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 VDCIHQYAKQPVSVGSASL 247
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Best Local Similarity 42.9%;
Matches 12; Conservative
                                                                                                                                                      hypothetical transmembrane
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Matches 10; Conserv
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A;Gene: SMb20040
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November 10, 2004, 14:50:40; Search time 46.9324 Seconds (without alignments) 343.270 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                        US-10-092-750-71
141
1 VSCWPSYLKYPLSTASASLLATQLKSIA 28
                                                                                                                                                                                                                                                                                                                                                                                   1825181 seqs, 575374646 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                         OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seg length: 200000000
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Perfect score:
Sequence:
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	Description		homo	homo	homo	homo	Q6nzj7 mus musculu	Aah66102 mus muscu	Q6gz70 homo sapien	Q6gz72 homo sapien	Q8zj53 yersinia pe	Q8d1g2 yersinia pe		Q9jgk4 meleagrid h		unculture		Q7n3s1 photorhabdu	Q8zvc8 pyrobaculum		Q8xrk7 ralstonia s			-		_	-	-			Q8vyg0 arabidopsis		Q6cx67 kluyveromyc
SUMMARIES	QI	į					Ī							-		Q7X329				_									QBITN3			Q9FF35	
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	Lengt		928	1831	1863	186	136	136	118	14	306	32(32(366	26	9	16(91	21:	24	353	57,	82	13.	12	24	32	32.	37	63	68	97	100
	Suery Query Match Length DB		40.4	40.4	40.4	40.4	37.6	37.6	36.5	36.5	36.2	36.2	36.2	36.2	35.5	35.5	35.5	35.1	34.8	34.8	34.8	34.8	34.8	34.4	34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0
	Score		57	57	57	57	53	53	51.5	51.5	51	51	51	51		.50	50	49.5	49	49	49	49	49	48.5	48	48	48	4.8	48	4.8	4.8	48	48
	Result No.		1	N	e	4	S	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20	30	31

	Q8tbn3 homo sapien	O35954 mus musculu	Aar06909 homo sapi	O00562 homo sapien	Q9bz73 homo sapien	Q8vull bacillus th	Q847c8 nodularia s	Q6xi00 drosophila	Aar10055 drosophil	Q9v169 drosophila	Q8rs30 comamonas a	Bac81981 comamonas	Q8blt8 mus musculu
Q6T7X3	Q8TBN3	035954	AAR06909	000562	Q9BZ73	QBVUL1	Q847C8	Oexioo	AAR10055	69NT69	Q8R530	BAC81981	QSBLT8
N	~	ď	0	N	N	N	~	~	N	~	N	~	0
1243	1243	1243	1243	1244	1244	1270	1299	180	180	190	298	298	345
34.0	34.0	34.0	34.0	34.0	34.0	34.0	34.0	33.7	33.7	33.7	33.7	33.7	33.7
4.8	48	48	4.8	48	48	48	48	47.5	47.5	47.5	47.5	47.5	47.5

ALIGNMENTS

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Query Match
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  COORER TO COORE SERVICE SERVIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.

TISSUB-Human spinal cord;
Ansorge W., Krieger B.,
Ansorge W., Krieger B.,
Mewes H.W., Well B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AL8322602; CAD89960.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                          Gaps
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Mame-MYCPBP;
Homo sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 37;
                                                                                                                                                                             Query Match 40.4%; Score 57; DB 2; Length 928; Best Local Similarity 50.0%; Pred. No. 18; Matches 10; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1831 AA; 205650 MW; C9CD64C74C4A907A CRC64;
                                                                                                                                         928 AA; 104964 MW; 7ACAD55D5204CB0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein DKFZp451C1717 (Fragment).
Name=DKFZp451C171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT; 1831 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Mismatches
                                                                                                                                                                                                                                                                                     241 IECWPSNSKYPLPVFSTFVL 260
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InterPro; IPR001194; DENN.
InterPro; IPR001194; DENN.
InterPro; IPR001194; DENN.
InterPro; IPR00113; uDENN.
Pfam; PP03455; dDENN; 1.
Pfam; PP03455; dDENN; 1.
Pfam; PF03456; uDENN; 1.
PROSITE; PS50947; DDENN; 1.
PROSITE; PS50947; DDENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 50.0%;
Matches 10; Conservative
                                                           PROSITE; PS50947; DDENN; 1.
PROSITE; PS50211; DENN; 1.
PROSITE; PS50946; UDENN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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Pfam; PF02141; DENN; 1.
Pfam; PF01535; PPR; 2.
Pfam; PF03456; uDENN; 1.
                                                                                                                        928
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SEQUENCE
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081VX2
ID 081VX
DT 01-M
DT 01-M
DT 01-M
DD C-M
GN Name
OS HOMO
OC BUKA:
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Righten R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
A platchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tochhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Jones S.J., Marra M.A.,
Jones S.J., Marra M.A.,
Todenztaion and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22788768; PubMed=12906859;
Semova N., Kapanadze B., Corcoran M., Kutsenko A., Baranova A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / Match 40.4%; Score 57; DB 2; Length 1863; Local Similarity 50.0%; Pred. No. 37; Local Similarity 50.0%; Pred. No. 37; DB 2; Mismatches 8; Indels
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Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC041706; AAH41706.1; -.
InterPro; IPR001194; DENN.
InterPro; IPR002815; PBN.
InterPro; IPR003815; PPR.1ike.
InterPro; IPR003113; unbENN.
Pfam; PP03455; dDENN; 1.
Pfam; PP03455; PPR; 2.
Pfam; PP03456; unbENN; 1.
Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-0CT-2003 (TrEMBLrel. 25, Created)
01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MRR-2004 (TrEMBLrel. 26, Last annotation update)
C-MYC promoter-binding protein IRLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1865 AA
                                                                                                                                                                                  MEDLINE=22388257; PubMed=12477932;
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PROSITE; PS50211; DENN; 1.
PROSITE; PS50946; UDENN; 1
SEQUENCE 1863 AA; 209220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE=Uterus;
                                                                                                            SEQUENCE FROM N.A.
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InterPro; IPR005113; uDENN.
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AAH66102;
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE TISSUE=Brain;

STRAIN=C57BL/6; TISSUE=Brain;

MEDINE=2538825; PubMed=1247932;

A Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Straubberg R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

A Alschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N. K.,

A Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B Distchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

B Erownstein M.J., Usdin T.B., Tochhiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,

A Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia S., Sanchez A.,

A Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Menses S.J., Marra M.A.,

T "Generation and initial analysis of more than 15,000 full-length human

The strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the strands of the 
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0
"Molecular cloning, structural analysis, and expression of a human
IRLB, WRC promoter-binding protein: new DENN domain-containing protein
family emerges.";
                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                             ò
                                                               EMBL, AFS34403, AAQ10514.1, ...

REMBL, AFS34403, AAQ10514.1, ...

InterPro; IPR005112; DENN.

R InterPro; IPR005183; PRN.

R InterPro; IPR005131; UDENN.

R Pfam; PF03455; DENN; 1.

R Pfam; PF03455; DENN; 1.

R Pfam; PF03456; UDENN; 1.

R PR05ITE; PS50947; DDENN; 1.

R PR05ITE; PS50947; DENN; 1.
                                                                                                                                                                                                                                                                                                                       DB 2; Length 1865; 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN=C55BL/6; TISSUE=Brain;
Strainsberg R.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT; 1369 AA
                                                                                                                                                                                                                                                                                                                       40.4%; Score 57; DB 50.0%; Pred. No. 38; iive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; BC066102; AAH66102.1; -. InterPro; IPR000345; CytC heme_BS. InterPro; IPR005112; dDENN. InterPro; IPR001194; DENN.
                                                                                                                                                                                                                                                                                                                                                                                                                                241 IECWPŚNSKYPLPVFSTFVL 260
                                                                                                                                                                                                                                                                                                                                                                                                1 VSCWPSYLKYPLSTASASLL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BC026996 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mouse cDNA sequences."
                                                 Genomics 82:343-354(2003).
                                                                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
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STRAIN-CSPEL6; TISSUE=Brain;

X STRAIN-CSPEL6; TUSSUE=Brain;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Klausherg R.L., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

X Klausher R.D., Collins F.S., Magner L., Shemmen C.M., Schuler G.D.,

A lischul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haiseh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haiseh F.,

A Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Haiseh F.,

A Bronsfein M.J., Usdin T.B., Toshiyuki S., Carninoi F., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Yillalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Shevchenko Y., Boutfard G.G.,

Raha S., Worley N., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Gnerzation and initial analysis of more than 15,000 full-length human

Man mouse C.DA sequences.
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                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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                                                                                                                                                                                                                                                                                                               Score 53; DB 2; Length 1369;
Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37.6%; Score 53; DB 2; Length 136
40.0%; Pred. No. 1.1e+02;
tive 4; Mismatches 8; Indels
                                                                                                                                                                                                                      NON TER 1 1
SEQUENCE 1369 AA; 149745 MW; 10F42885A240E087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1369 AA; 149745 MW; 10F42885A240E087 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-2004 (TrEMBLrel. 27, Created)
C2-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
EC02696 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT; 1369 AA
                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
Pfam, PF01455; dDENN, 1.
Pfam, PF02141, DBNN, 1.
Pfam, PF03145, uDENN, 1.
PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
PROSITE; PS50947, DDENN, 1.
PROSITE; PS50941, DDENN, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 229 IECWPAQTKYPVPVFSTFVL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             229 IECWPAQTKYPVPVFSTFVL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 VSCWPSYLKYPLSTASASLL 20
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STRAIN-C57BL/6; TISSUE=Brain;
                                                                                                                                                                                                                                                                                                        37.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; BC066102; AAH66102.1;
NON_TER 1 1
                                                                                                                                                                                                                                                                                                                                                                              8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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7

Gaps

7:

6; Indels

147;

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Query Match 36.5%; Score 51.5; DB 2; Length Best Local Similarity 51.7%; Pred. No. 17; Matches 15; Conservative 1; Mismatches 6; Indels
               Probom; PD000035; ZnF_C4steroid; 1.
SMART; SM00399; ZnF_C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 147 AA; 16602 MW; F03F83F41D00D493 CRC64;
                                                                                                                                                                                                                                                                       96 WKSVTSYSIPLSVSKHKTSSAGLFATQLK 124
                                                                                                                                                                                                                                       4 WPSYLKY--PLS----TASASLLATQLK 25
PRINTS; PR00350; VITAMINDR.
                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Complete proteome. SEQUENCE 306 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yersinia pestis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPRO
Pfam; PF01052;
                                                                                                                                                                                                                                                                                                                                                                                     Q8ZJ53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08D1G2
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Q8D1G2
ID Q8D1G
AC Q8D1G
DT 01-MADT 01-MA
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Q8ZJ53
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Lamba J.K., Lamba V., Yasuda K., Lin Y.S., Assem M., Thompson E.,
Strom S., Schuetz E.G.;
                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lamba J.K., Lamba V., Yasuda K., Lin Y.S., Assem M., Thompson E., Strom S., Schuetz E.G., "Expression of CAR splice variants in human tissues and their
                                                                                                                                                                                                                                                                                                                                                                                                          US-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Constitutive androstane receptor SV20 (Constitutive androstane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 28, Last annotation update)
CONSTITUTE and FOOTER PROSPERS FOOTER STATEMENT OF THE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
36.5%; Score 51.5; DB 2; Length 118;
Best Local Similarity 51.7%; Pred. No. 13;
Matches 15; Conservative 1; Mismatches 6; Indels 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00399; ZnF C4; 1.
DNA-binding; Metal-Dinding; Nuclear protein; Receptor;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 118 AA; 13460 MW; E2793D4F3368BB46 CRC64;
                                                                                 118 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 147 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 WPSYLKY--PLS-----TASASLLATQLK 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 WKSVTSYSIPLSVSKHKTSSAGLFATÖLK 95
                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, AY572822, AAT47175.1; -.
InterPro; IPR00034; VALD receptor.
Interpro; IPR001628; Znf_C4steroid.
Pfan; PF00105; Zf-C4; 1.
PR1NTS; PR00047; STROIDFINGER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   functional consequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                           Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sabiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor SV17).
Name=NR113;
                                                                                                                                                                                                                            Name=NR113;
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                                                                                   06GZ70
                                          RESULT 7
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                                                            06GZ70
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STRAINS-CO-92 North Contentalis;
STRAINS-CO-92 North Contentalis;
STRAINS-CO-92 North Contentalis;
MEDLINE-21470413; PubMed=11886360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.E., Titball R.W., Holden M.T.G.,
Prentice M.B., Sebaina M., James K.D., Churcher C.M., Mungall K.L.,
A Baker S. Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
Chillingworth T., Cronin A., Davis P., Dougan G.,
Chillingworth T., Cronin A., Davis P., Marlyanev A.V.,
Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
Genome sequence of Yersinia pestis, the causative agent of plague.";
In ature 413:52-527(2001).
In Nature 413:52-527(2001).
In Nature 413:52-527(2001).
In Rembi, AJ41411; CAC8913.1;
C. -: SIMILARIY: Belongs to the flin/mopA/spao family.
EMBL, AJ41411; CAC8913.1;
C. -: SIMILARIY: Remotor activity; IEA.
RO; GO:0009125; P:chimotaxis; IEA.
RO; GO:0001539; P:chimotaxis; IEA.
R GO; GO:0001539; P:chimotaxis; IEA.
R InterPro; IPR001172; Flagellar motility; IEA.
R InterPro; IPR001172; Flagellar Flin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                              Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
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36.2%; Score 51; DB 2; Length 306;
Best Local Similarity 43.5%; Pred. No. 43;
Matches 10; Conservative 4; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     306 AA; 33423 MW; 964683C5A79783A4 CRC64;
                                                                      01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-UNJ-2003 (TrEMBLrel. 24, Last annotation update)
Type II secretion system apparatus protein.
OrderedLocusNames=YP00269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QBDIG2; Q74XJ4;
01-MbR-2003 (TrEMBLrel. 23, Created)
01-MbR-2003 (TrEMBLrel. 23, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               320 AA.
306 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 SCWPSYLKYPLSTASASLLATQL 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SCWQHWLNTTLATDNPQLLAAEL 63
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00956; FLGMOTORFLIN. ProDom; PD001777; SpoA; 1.
                                                                                                                                                                                                                                                                                                                                                                          Enterobacteriaceae, Yersinia
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Gaps

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Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

Lubrited (OCT-1999) to the EMBL/GenBank/DDBJ databases.

Lubrited (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-i-SIMILARITY: Belongs to the bZIP family.

EMBL; AB033119; BAA33716.1; -.

EMBL; AB033119; BAA33716.1; -.

EMBL; AB003317; F:DMA binding; IEA.

GO; GO:00006357; F:DMA binding; IEA.

R GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.

INTERPRO; IPR008937; Leuzip Foo.

R InterPro; IPR008937; Leuzip Foo.

R InterPro; IPR004937; TE LEUZIP FOO.

R PROSTTE; PR00101; bZIP; 1.

R PROSTTE; PR00103; BZIP; 1.

R RRINTS; PR000136; BZIP; 1.

R RRSTTE; PR00136; BZIP; 1.

R RRSTTE; PR001036; BZIP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=96127529; PubMed=8590279;
Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
Sugiura M., Tabata S.;
Sequence analysis of the genome of the unicellular cyanobacterium
Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.2%; Score 51; DB 2; Length 394; 50.0%; Pred. No. 57;
                               Length 320;
                                                                                       Indels
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OrderedicousNames=sIr1033;
Synechocystis (strain PCC 6803).
Synechocystis Asacteria, Chrococcales, Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Meleagrid herpesvirus 1 (MeHV-1) (Turkey herpesvirus)
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Marek's disease-like viruses.
NCBI_TaxID=10390;
                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2000 (TrEMBLrel, 15, Created)
01-0CT-2000 (TrEMBLrel, 15, Last sequence update)
01-MAR-2004 (TrEMBLrel, 26, Last annotation update)
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Last annotation update)
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                            Score 51; DB 2;
Pred. No. 45;
4; Mismatches
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                                                                                                                                                2 SCWPSYLKYPLSTASASLLATQL 24
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                            Query Match
Best Local Similarity 43.5%;
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 50.0
nes 9, Conservative
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                                                                                                                                                                                                                                                                                             RESULT 12
Q9JGK4
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P73143
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STRAIN=91001 / Biovar Mediaevalis;
SONG Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
                                                                                                                                                                                                                                                                                                                                                         Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P., Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V., Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R., Perry K.D.; Genome sequence of Yersinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).
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STRAIN=91001 / Biovar Mediaevalis;

STRAIN=91001 / Biovar Mediaevalis;

STRAIN=91001 / Biovar Mediaevalis;

SONG Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou J.

Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Huang P.,

Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,

Yang R.;

Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.

EMBL; AR011128; AAS60695.1; --

SEQUENCE 320 AA; 34947 MW; 4FIE84019C908A41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
                                                                                                                                                   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Yersinia.
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Lebumited (APR-2003) to the EMBL/GenBank/DDBJ databases.
Lebumited (APR-2003) to the flin/mopA/spaO family.
Rebul, AB013654; AAM84117.1; ...
Rebul, AB017128; AAS60655.1; ...
Repul, AB017128; AAS60655.1; ...
Repul, AB017128; AS60655.1; ...
Repul, AB017128; Repular basal body (sensu Bacteria); IEA.
Recolomosance activity; IEA.
Recolomosance activity activity activity; IEA.
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Recolomosance activity activity activity activity activity.
Recolomosance activity activity activity activity activity activity.
Recolomosance activity 
Recolomosance activity a
01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Putative type III secretion system component (Type III secretion
System apparatus protein)
Name=fliN1; OrderedLocusNames=YP0424, y0529;
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34947 MW; 4F1E84019C908A41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AASG0695,
24-MRA-2004 (TrEMBLrel. 27, Created)
24-WAR-2004 (TrEMBLrel. 27, Last sequence update)
04-MAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 51; DB 2;
Pred. No. 45;
4; Mismatches
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FLIN1 OR YP0424.
Yersinia pestis.
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STRAIN=KIMS / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
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Matches 10; Conserv
                                                                                                                       Yersinia pestis.
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                                                                         STRAIN=PCC6803;
MEDLLINE=97061201; PubMed=8905231;
MEDLLINE=97061201; PubMed=8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hisosuchi T., Mateuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
Tabata S.;
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                                                                                                                                                                                      "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).
EMBL; D90904; BAA17169.1; -.
PIR; S75255; S75255.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-22983092; PubMed=14617179; MEDLINE-22983092; PubMed=14617179; Medline-22983092; PubMed=14617179; Modified R.O., Treusch A.H., Eck J., Schleper C.; Carleper C.; Carleper C.; Carleper C.; Carleper C.; Acidobacteria form a coherent but highly diverse group within the macterial domain: evidence from environmental genomics."; Mol. Microbiol. 50:563-575 (2003).

EMBL, AX281354; AAPS8535.1;
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                                                                                                                                                                                                                                                                                                                                                                  Query Match 35.5%; Score 50; DB 2; Length 565; Best Local Similarity 36.0%; Pred. No. 1.2e+02; Matches 9; Conservative 7; Mismatches 9; Indels
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35.5%; Score 50; DB 2; Length 608;
Best Local Similarity 52.4%; Pred. No. 1.38+02;
Matches 11; Conservative 2; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 608 AA; 64406 MW; 2C88C8BE9BF21AA9 CRC64;
                                                                                                                                                                                                                                                                                                                                   565 AA; 64181 MW; 1C569961D4ACBF90 CRC64;
region from map positions 64% to 92% of the genome.", DNA Res. 2:153-166(1995).
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Last annotation update)
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
RT-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical protein. or man amiocation upo uncultured Acidobacteria bacterium.

Bacteria; Acidobacteria; environmental samples.

NCBI_TaxID=171953;
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Venturia inaequalis (Apple scab fungus).
Mitochondrion.
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01-OCT-2003 (TrEMBLrel. 25,
01-OCT-2003 (TrEMBLrel. 25,
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                                                        SEQUENCE FROM N.A.
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047500
AC 04750
AC 04750
BT 01-JU
BT 01-JU
BT NT-II
GN NAME:
CS Ventu
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Q7X329
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Zheng D., Koller W.; "Characterization of the mitochondrial cytochrome b gene from Venturia
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BMBL, AF004559, AAB95256.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005739; C:mitochondrion; IEA.

GO; GO:0003721; F:RNA binding; IEA.

GO; GO:0003723; F:RNA binding; IEA.

GO; GO:0003801; P:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003801; P:RNA-directed DNA polymerase activity; IEA.

GO; GO:0003801; P:RNA-directed DNA replication; IEA.

GO; GO:0005789; P:RNA-dependent DNA replication; IEA.
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Pfam; PF00043; Cytcchrom B N; 1.
Pfam; PF01348; Introm aturae2; 1.
Pfam; PF00178; RVT; 1.
Pfam; PF00078; RVT; 1.
Mitochondrion; RNA-directed DNA polymerase; Transferase; SEQUENCE 760 AA; 85883 MW; 6180C1D5E6C55EA2 CRC64;
Pleosporales, Venturiaceae, Venturía.
NCBI_TaxID=5025;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR005797; Cytb b6 N.
InterPro; IPR000577; FGGY_kin.
InterPro; IPR000442; Intron_maturse2.
                                                                                                                                         STRAIN=S-56-88;
MEDLINE=98041928; PubMed=9371888;
                                                                                                    SEQUENCE FROM N.A.
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Search completed: November 10, 2004, 15:53:35
Job time : 49.0093 secs

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sequence 41366, A
Sequence 5582, A
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 5288, Ap
Sequence 28143, A
Sequence 724, App
Sequence 121, App
Sequence 10, Appli
Sequence 10, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 10, Appli
Sequence 21, Appli
Sequence 21, Appli
Sequence 25, Appli
Sequence 25, Appli
Sequence 25, Appli
     Sequence 1
Sequence 1
Sequence 1
Sequence 4
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/08459146
; Sequence 3, Application US/08459146
; Patent No. 5866405
; GENERAL INFORMATION:
APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION Genetically Engineered Transmissible
TITLE OF INVENTION Genetically Engineered Transmissible
TITLE OF INVENTION GENETICAL TRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3165;
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CZEP: 0/110
CZEP: 0/110
CZEP: 0/110
MEDIUM TYPE: Floppy disk
COMPUTER: END PC compatible
COMPUTER: END PC compatible
COPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHTION DATA:
APPLICATION NUMBER: US/08/459,146
FILING DATE: 02-JUN-1995
CLASSIPICATION NUMBER: US 07/832,117
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
FILING DATE: 06-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: ROSEMEN, CATHORINER: 8589
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-530
INFORMATION FOR SED ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 3165 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: ALLOR OF TAXACTERISTICS:
TYPE: ALLOR OF TAXACTERISTICS:
TYPE: ALLOR OF TAXACTERISTICS:
TYPE: ALLOR OCIDE
TYPE: AL
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US-08-415-818-12

US-08-894-216-12

PCT-US96-01444-136

US-09-270-767-41366

US-09-252-991A-21407

US-08-315-468-4

US-09-173-581-1

US-09-173-581-1

US-09-173-581-1

US-09-107-32A-5288

US-09-252-991A-2843

US-09-252-91A-2843

US-09-252-91A-2843

US-09-252-91A-2843

US-09-114-01C-3512

US-09-869-388-10

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     US-08-459-146-3
        Query Match
     Sequence 3, Appli
Sequence 4316, Ap
Sequence 9781, Ap
Sequence 9781, Ap
Sequence 5320, Ap
Sequence 5310, Ap
Sequence 516, App
Sequence 516, App
Sequence 2785, A

Sequence 2788, Ap
Sequence 2788, Ap
Sequence 2788, Ap
Sequence 2788, Ap
Sequence 2819, Appl
Sequence 2813, Appl
Sequence 2813, Appl
Sequence 215, Appl
Sequence 216, Appl
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Seguence 989, App
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Appli
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181.178 Million cell updates/sec
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                                                                                                                                                                                 2004, 13:44:14 ; Search time 8.78491 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Description
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/BCOMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                           GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-448-0005-3

US-09-148-0001-4332

US-09-134-0010-4332

US-09-134-0010-4332

US-09-134-0010-4332

US-09-328-352-5907

US-09-328-352-5907

US-09-0489-0330-13740

US-09-03-28-991A-29785

US-09-02-28-991A-29785

US-09-134-0000-6358

US-09-134-0010-6358

US-09-134-0010-6358

US-09-134-0010-6358

US-09-134-0010-6358

US-09-134-0010-6358

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US-09-079-030-11

US-09-079-030-11

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US-09-079-030-11

US-09-079-030-11

US-09-079-030-11

US-09-079-030-11

US-09-079-030-11

US-09-079-030-11

US-09-078-080-11

US-09-078-080-11

US-09-078-080-11

US-09-538-092-84-3
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1 VHNFGRHWGLPLSFLLNYPLFLSP 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             OM protein - protein search, using sw model
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length: 2000000000
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Match Length
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Perfect score:
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Maximum DB seq
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, TYPE: PRT
, ORGANISM: Staphylococcus epidermidis
US-09-134-001C-4332
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                                                                                                                                                                                                                                                                                                                                                             4 FGRHWGLPLS -- FLLNYPLFLS 23
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                                                                                                                                                                                                                    ORGANISM: Enterococcus faecalis
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Best Local Similarity
Matches 8; Conserv
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US-09-489-039A-9781
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; Sequence 4816, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
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                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc. STREET: 340 Kingsland Street CITY: Nutley STATE: New Jersey COUNTRY: U.S.A.
                                                                                                                                                                                                                                          GENERAL INFORMATION:

APPLICANT: Choi, Gil Ho
APPLICANT: Nuss, Donald Lee
TITLE OF INVENTION: Genetically Engineered Transmissible
TITLE OF INVENTION: Hypovirulence
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc
                     Indels
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MEDIUM TYPE: RIOPY disk

MEDIUM TYPE: RIOPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 07/832,117

FILING DATE: 06-FBS-1992

ATTORNEY/AGENT INFORMATION:

NAME: ROSEMAN, Catherine R

REGISTRATION NUMBER: 8589

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION ON 33:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:
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ORGANISM: parasitica)
Best Local Similarity 54.2%; Pred. No. 86;
Matches 13; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 VRNTGIH-GLPGDFLSNYPRLPTP 536
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                                                          1 VHNFGRHWGLPLSFLLNYPLFLSP 24
                                                                                                                                                                                                   Sequence 3, Application US/08459065
Patent No. 5882642
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TOPOLOGY: 11-2

OLFOTT
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MOLECULE TYPE: protein
HYPOTHETICAL: NO
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US-08-459-065-3
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Sequence 433.2, Application US/09134001C
Sequence 433.2, Application US/09134001C
Sequence 433.2, Application US/09134001C
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: BPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-108-14
NUMBER OF SEQ ID NOS: 5674
LENGTH: 287
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Squares 9781, Application US/09489039A
Squares 9781, Application US/09489039A
Squares 9781, Application US/09489039A
GENERAL INFORMATION:
APPLICANT GATY Breton et. al
APPLICANT OF INVENTION:
TITLE OF INVENTION:
PREMEMORY OF STORE ST
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TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1996-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR PILING DATE: 1997-08-15
NUMBER: OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4816
LENGTH: 470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

36.2%; Score 50; DB 4; Length 470;
Best Local Similarity 40.9%; Pred. No. 25;
Matches 9; Conservative 6; Mismatches 5; Indels
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APPLICANT: Gary Breton et. al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA TITLE OF INVENTION: DREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS CURRENT EFFERENCE: 2703-2004601.

CURRENT APPLICATION NUMBER: US/09/489,039A

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342
                                                                                                                                                                                                                                                                                                                                                        7
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| Patent No. 6635623
| GENERAL INFORMATION
| GENERAL INFORMATION
| APPLICANT: Hoogeveen, Ron G. APPLICANT: Moore, Paul J. InfoRPOTONI MOORE, Paul J. ITLE OF INVENTION: UPCTORS FOR TRANSFECTION OF EUKARYOTIC CELLS NUMBER OF SEQUENCES: 229
| CORRESPONDENCE ADDRESS: Annold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                     18;
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                                                                                                                                                                                                                                                                                                              Length 435;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                    249 NFRLHWRDRGLPLLFVEGFLLMGAFVTLFNYIGYRLMMSP 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER, TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: CONCURRENT! Herewith
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                             -----LNYPLFLSP
                                                                                                                                                                                                                                                                                                              DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 4;
Pred. No. 85;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                              Score 48;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MGMIJIAIN, NADOBIA R.
RECISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:
                                                                                                                                                                                                                                               ) ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 216: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34.8%;
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Best Local Similarity 32.55,
Best Local 13; Conservative
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Best Local Similarity 54.5'
Matches 12; Conservative
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: USA
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COUNTRY: US/
ZIP: 77210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
US-09-079-030-216
                                                                                                                                                                                      SEQ ID NO 13740
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                                                                                                                                                                                                                                TYPE: PRT
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APPLICANT: GAIY L. BRECON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
EENGTH: 420
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                                                                                                                                                                                                                     Sequence 2320, Application US/09710279
Patent No. 6703492
GENERAL INFORMATION
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
FILE REFERENCE: P03480US
CURRENT APPLICATION NUMBER: US/09/710,279
CURRENT FILING DATE: 2000-11-09
PRIOR APPLICATION NUMBER: 6/164,258
PRIOR PLING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: PATENTIN VET. 2.1
                                             Gaps
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OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-710-279-2320
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    Length 287;
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34.8%; Score 48; DB 4; Length 287;
Best Local Similarity 45.5%; Pred. No. 28;
Matches 10; Conservative 3; Mismatches 9; Indels
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                                           Indels
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  Score 48; DB 3;
Pred. No. 28;
3; Mismatches
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Pred. No. 43;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 13740, Application US/09489039A; Patent No. 6610836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5907, Application US/09328352 Patent No. 6562958
                                                                                3 NFGRHWGLPLSFLLNYPLFLSP 24
                                                                                                          40 NLGEGSIGLSLILNYTLGISP 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Acinetobacter baumannii
US-09-328-352-5907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 FGRHWGLPLSFLLNYPLFLS 23
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45.0%;
Query Match
Best Local Similarity 45.5%;
Matches 10; Conservative
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ORGANISM: Artificial Sequence
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Best Local Similarity 45.0°
Matches 9; Conservative
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US-09-489-039A-13740
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APPLICANT: Tao, Jianshi
APPLICANT: Qui, Yan
APPLICANT: Qui, Yan
APPLICANT: Shan, Xiaoyu
APPLICANT: Schimel, Paul R.
ITLE OF INVENTION: Helicobacter Aminoacyl-tRNA Synthetase
TITLE OF INVENTION: Proteins, Nucleic Acids and Strains Comprising Same
VUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                            Query Match
34.1%; Score 47; DB 4; Length 335;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 8; Conservative 4; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5349
LENGTH: 335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/08451715A Patent No. 5801013
                                                                                                                                  TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-5349
                                                                                                                                                                                                                                                                                                                               230 YWLWPLAYLTPFPLFL 245
                                                                                                                                                                                                                                                                                                    7 HWGLPLSFLLNYPLFL 22
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CITY: Lexington
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , MOLECULE TYPE: protein US-08-451-715A-2
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US-09-248-796A-16735

J Sequence 16735, Application US/09248796A

Sequence 16735, Application US/09248796A

PAPLICANT: Kaith Weinstock et al

APPLICANT: Kaith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196-132

CURRENT APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-02-13

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208

SEQ ID NO 16735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:

Pacent No. 6551795

GENERAL INFORMATION:

Pacent No. 6551795

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TITLE OF INVENTION:

ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPREBENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR FILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-17

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 29785
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) Patent No. 6562958
) GENERAL INFORMATION:
) APPLICANT: GATY L. Breton et al.
) TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER;
) TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
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34.1%; Score 47; DB 4; Length 273;
Best Local Similarity 40.0%; Pred. No. 37;
Matches 8; Conservative 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 4; Length 114;
Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; Indels
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        320 GFPLKLTGKIDFLNNYALFLSP 341
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-29785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 34.4%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-16735
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US-09-252-991A-29785
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APPLICANT: LYAN DOMOCATED:
APPLICANT: LYAN DOMOCATED:
APPLICANT: LYAN DOMOCATED:
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTERCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT PILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE PACENTIN VEXEION 3.1
SEQ ID NO 6358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 43, Application US/09079030

Patent No. 6635623

GENERAL INFORMATION:

APPLICANT: Geuvera, Jr., Juan G.

APPLICANT: Hoogeveen, Ron C.

APPLICANT: Moore, Paul J.

TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
TITLE OF INVENTION: USCOPER FOR TRANSFECTION OF BUKARYCTIC CELLS
NUMBER OF SEQUENCES: 229

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STREET: P.O. Box 4433

COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DATE PC COMPATIBLE
COMPATER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: CONCULTENTLY HEYEWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
US-09-134-000C-6358
; Sequence 6358, Application US/09134000C
; Patent No. 6617156
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NAME: McMilian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 100 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6358
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69.2%;
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Best Local Similarity
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US-09-079-030-43
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US-09-079-030-43
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Sequence 78181, A Sequence 19181, A Sequence 17957, Sequence 17886, A Sequence 10165, A Sequence 10165, A Sequence 10165, A Sequence 10155, A Sequence 26558, A Sequence 26763, A Sequence 2763, A Sequence 2763, A Sequence 24780, Sequence 24780, Sequence 259248, Sequence 255248, Sequence 355684, 
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Sequence 36420, A
Sequence 7061, Ap
Sequence 7061, Ap
Sequence 56081, Ap
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Publication No. US20030032157A1

GENERAL INFORMATION:
APPLICANT: Hammond, Philip W.
APPLICANT: Alphin, Julia
APPLICANT: Alphin, Julia
APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1
FILE REFERENCE: 50036/050002
CURRENT APPLICATION NUMBER: US/10/092,750
CURRENT APPLICATION NUMBER: US 60/274,526
PRIOR APPLICATION NUMBER: US 60/274,526
NUMBER OF SEQ ID NOS: 253
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 24
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6 US-10-437-963-187128

5 US-10-424-599-194663

5 US-10-424-599-194663

5 US-10-424-599-194663

5 US-10-424-599-270867

5 US-10-282-122A-59419

6 US-10-282-122A-59419

6 US-10-282-122A-62865

5 US-10-282-122A-6258

6 US-10-282-122A-6558

7 US-10-282-122A-65785

5 US-10-282-122A-65785

5 US-10-282-122A-6785

5 US-10-282-122A-6785

5 US-10-425-114-40755

7 US-10-425-115-314-40755

7 US-10-425-115-314-40755

7 US-10-425-115-314-40763

5 US-10-425-115-314-40763

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7 US-10-425-115-314-709

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-092-750-51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-092-750-51
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US-09-797-097-2
       \begin{matrix} \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{0} & \mathbf{0} & \mathbf{0} & \mathbf{0} \\ \mathbf{0} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{0} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} \\ \mathbf{d} & \mathbf{d} & \mathbf{d} \\ \mathbf{d} \\ \mathbf{d} & \mathbf{d} \\ \mathbf{d} \\ \mathbf{d} & \mathbf{d} \\ \mathbf{d} \\ \mathbf{d} \\ \mathbf{d} & \mathbf{d} \\ \mathbf{d} 

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Sequence 2, Appli
Sequence 183840,
Sequence 104238,
Sequence 60769, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 49, Appli
Sequence 78114, A
Sequence 216105,
Sequence 216105,
                                                                                                                                                                                                                                                   November 11, 2004, 01:28:30; Search time 27.7585 Seconds (without alignments) 305.399 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUBLPSpp:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW PUBLPSpp:*

3: /cgn2_6/ptodata/1/pubpaa/NSO6_NEW PUBL pep:*

4: /cgn2_6/ptodata/1/pubpaa/USO6_NEW PUBL pep:*

5: /cgn2_6/ptodata/1/pubpaa/USO7_NEW PUBL pep:*

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11: /cgn2_6/ptodata/1/pubpaa/USO8_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUBL.pep:*

12: /cgn2_6/ptodata/1/pubpaa/USO9_NEW PUBL.pep:*

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16: /cgn2_6/ptodata/1/pubpaa/USO10C_PUBCOMB.pep:*

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18: /cgn2_6/ptodata/1/pubpaa/USO10NEW PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO10NEW PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO10NEW PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/USO0NEW PUB.pep:*

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19: /cgn2_6/ptodata/1/pubpaa/USO0NEW PUB.pep:*
                                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-09-797-097-2

5 US-10-424-59-183840

6 US-10-437-963-104238

5 US-10-282-122A-60769

4 US-10-369-736-3

4 US-10-369-738-3

4 US-10-369-738-3

4 US-10-369-738-3

5 US-10-282-122A-78114

5 US-10-282-122A-78114

6 US-10-282-125A-78114

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1 VHNFGRHWGLPLSFLLNYPLFLSP 24
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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APPLICANT:
AVELICANT:
AVELICANTIN: AND H.
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: US/10/282,122A
CURRENT PAPLICATION NUMBER: 00/3-22-0
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-26
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PRIOR PLING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-09-09
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-29
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2001-02-09
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                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: unsure
COCATION: (1)...(88)
OTHER INFORMATION: unsure at all Xaa locations
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_101591C.1.pep
US-10-437-963-104238
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39.1%; Score 54; DB 16;
Best Local Similarity 56.5%; Pred. No. 5.1;
Matches 13; Conservative 1; Mismatches 3
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 104238
LENGTH: 88
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 60769, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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; ORGANISM: Listeria monocytogenes
US-10-282-122A-60769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Olisen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Tyskind, Judith
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Trawick, John
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1
SEQ ID NO 60769
LENGTH: 461
                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-282-122A-60769
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Sequence 104218, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: Experiment of the control                                                                          APPLICANT: Howard, John
TITLE OF INVENTION: Expression Cassettes and Methods of Delivery of Animal Vaccines
FILE REFERENCE: P00246US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 183840, Application US/10424599
| Sequence 183840, Application US/10424599|
| Sequence 183840, Application US/20040031072A1 |
| Sequence 183840, Application No. US20040031072A1 |
| Sequence 183840, Application No. US20040031072A1 |
| APPLICANT: La Rosa Thomas J |
| APPLICANT: Zhou Yihua |
| APPLICANT: Zhou Yihua |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With |
| TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement |
| CURRENT APPLICATION NUMBER: US/10/424,599 |
| CURRENT PILING DATE: 2003-04-28 |
| NUMBER OF SEQ ID NOS: 285684
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39.5%; Score 54.5; DB 15; Length 374;
Best Local Similarity 52.4%; Pred. No. 19;
Matches 11; Conservative 4; Mismatches 5; Indels 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 43.5%; Score 60; DB 9; Length 1447; Best Local Similarity 60.0%; Pred. No. 12; Matches 12; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
, ORGANISM: Transmissible Gatroenteritis Virus Spike protein
US-09-797-097-2
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_137021C.1.pep
US-10-424-599-183840
                                                                                                                                                                                    CURRENT APPLICATION UNDER: US/09/797,097
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 08/529,006
PRIOR FILING DATE: 1995-09-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin version 3.0
LENGTH: 1447
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                                APPLICANT: All, Benjamin
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LENGTH: 374
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Gaps
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                           Sequence 3, Application US/10369738
; Sequence 3, Application US/10369738
; Publication No. US20030180306A1
; GENERAL INPORMATION:
; APPLICANT: HILL, VENNIFER J.
; TITLE OF INVENTION: FOLLSTATIN DOMAIN CONTAINING PROTEINS
; FILE REPRENCE: 08702.0014-00
; CURRENT FILING DATE: 2003-02-21
; PRIOR PILING DATE: 2003-02-21
; PRIOR PILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; PRIOR FILING DATE: 2002-02-21
; RIOR FILING DATE: 2002-12-20
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 571
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US-10-369-738-49

US-10-369-738-49

SQUENCE 49, Application US/10369738

PUBLICATION NO. US2003180306A1

GENERAL INPORMATION:

APPLICANT: HILL, JENNIFER J.

TITLE OF INVENTION: POLLSTATIN DOMAIN CONTAINING PROTEINS

FILE REFERENCE: 05702,0014-00

CURRENT FILING DATE: 2003-02-21

PRIOR APPLICATION NUMBER: 05/357,846

PRIOR PILING DATE: 2002-02-21

PRIOR APPLICATION NUMBER: 60/434,645

PRIOR FILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PARCHEIN Ver. 2.1

SEQ ID NO 499
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Pred, No. 34;
0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 39.1%; Score 54; DB 14; Length 571; Best Local Similarity 57.9%; Pred. No. 34; Matches 11; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 78114, Application US/10282122A; Publication No. US20040029129A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 HNFGRHWGLPLSFLLNYPL 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 HRFWFHWGLLLLLLEAPL 25
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 57.9
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: Mus sp. US-10-369-738-3
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US-10-282-122A-78114
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                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
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Sequence 3, Application US/10369736;
Publication No. US20030162714A1;
GENERAL INFORMATION:
APPLICANT: HILL, JENNIFER J.
APPLICANT: HILL, JENNIFER J.
TITLE OF INVENTION: FOLLISTATIN DOMAIN CONTAINING PROTEINS;
FILE REFERENCE: 08702.0015-00;
CURRENT APPLICATION NUMBER: US/10/369,736;
CURRENT FILING DATE: 2003-02-21;
PRIOR FILING DATE: 2002-02-21;
PRIOR PILING DATE: 2002-12-20;
PRIOR PILING DATE: 2002-12-20;
NUMBER OF SEQ ID NOS: 53;
SOFTWARE: PATENTIN VET: 2.1
SEQ ID NO 3
LENGHH: 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 39.1%; Score 54; DB 15; Length 461; Best Local Similarity 40.9%; Pred. No. 28; Matches 9; Conservative 8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 39.1%; Score 54; DB 14; Length 571; Best Local Similarity 57.9%; Pred. No. 34; Matches 11; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 39.1%; Score 54; DB 14; Length 571; Best Local Similarity 57.9%; Pred. No. 34; Matches 11; Conservative 0; Mismatches 8; Indels
                                                                               4 FGRHWGLPLSFL--LNYPLFLS 23
                                                                                                         76 FGRKWGARVAWLYWINYPIWMA 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Mus sp.
US-10-369-736-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Mus sp. US-10-369-736-49
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US-10-437-963-185786

i Sequence 185786

j Publication No. US20040123343A1

j GENERAL INFORMATION:

j APPLICANT: La Rosa, Thomas J.

j APPLICANT: Zhou, Yihua

j APPLICANT: Boukharcov, Andrey A.

j APPLICANT: Boukharcov, Andrey A.

j APPLICANT: Boukharcov, Andrey A.

j APPLICANT: Li, Ping

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With

j TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

j FILE REFERENCE: 36-21(53221)B

CURRENT APPLICATION NUMBER: US/10/437,963

j CURRENT PILING DATE: 2003-05-14

NUMBER OF SEQ ID NOS: 204966

j SEQ ID NO 185786

j EBNCTH: 284

m. TOBE OF THE SEQ ID NOS: 204966

j EBNCTH: 284
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TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERDICE: ELITRA.034A
FILE REPERDICE: ELITRA.0340
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT PILING DATE: 2003-02-20
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                 Score 51; DB 15; Length 61;
Pred. No. 9.5;
                                                                          7; Indels
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US-10-437-963-185786
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Pred. No. 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)..(284)
OTHER INFORMATION: unsure at all Xaa locations
                 137.0%; Score 51; DB ilarity 52.6%; Pred. No. 9.5; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 57060, Application US/10282122A Publication No. US20040029129A1
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
                                                                                                                                  5 GRHWGLPLSFLLNYPLFLS 23
                                                                                                                                                                                  3 GLIWHVPYTFALKRPLFLS 21
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APPLICANT: Wang, Liangeu
APPLICANT: Randio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Maselbeck, Robert
APPLICANT: Obleen, Kari
APPLICANT: Cyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 37.0%;
1 Similarity 50.0%;
12; Conservative
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Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                 Query Match
Best Local Similarity
Matches 10; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
NAME/KEY: unsure
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APPLICANT:
APPLICANT:
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Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
APPLICANT:
Cao Yongwei
TITLE OF INVENTION:
Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION:
PILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE:
CURRENT FILING DATE:
2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 216105
LENGTH: 61
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PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR FILING DATE: 2000-03-21

PRIOR PULING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR APPLICATION NUMBER: 60/2030,347

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-06

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-09-09

PRIOR FILING DATE: 2000-10-23

PRIOR PELING DATE: 2000-10-23

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-11-27

PRIOR PELING DATE: 2000-10-29

PRIOR FILING DATE: 2000-12-29

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-09

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308

PRIOR PRIOR PRIOR PRIOR APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                             TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA-034A CURRENT APPLICATION NUMBER: US/10/282,122A CURRENT FILING DATE: 2003-02-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   242 NFKLHWRDSGLPLLFAEGFLIMGGVVTLFNYIGYRLLDGPYYLSP 286
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, OTHER INFORMATION: Clone ID: PAT_MRT3847_37172C.1.pep

US-10-424-599-216105
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1; Mismatches
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35.6%;
Haselbeck, Robert
                                                                                                       Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                          Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 37.3
Best Local Similarity 35.6
Matches 16; Conservative
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ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-282-122A-78114
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APPLICANT:
APPLICANT:
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Sequence 194663, Application US/10424599;
Publication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 194663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 49.5; DB 15; Length 158;
Pred. No. 41;
4; Mismatches 9; Indels 13
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US-10-424-599-194663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 VHNEGRHWGLP-----LSFLLNYPLFLSP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: unsure
LCARTION: (1)..(158)
LHER INFORMATION: unsure at all Xaa locations
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search completed: November 11, 2004, 02:43:07 Job time: 28.8085 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 35.9%;
Best Local Similarity 29.7%;
Matches 11; Conservative 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT ORGANISM: Glycine max
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Sequence 187128, Application US/10437963

Publication No. US20040123343A1

GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Acou, Yinua
APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 187128
LENGTH: 1043
LENGTH: 1043
PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-23

PRIOR PILING DATE: 2000-05-66

PRIOR PILING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-06

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-09-09

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-10-23

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-11-27

PRIOR PLING DATE: 2000-12-22

PRIOR PLING DATE: 2001-12-27

PRIOR PLING DATE: 2001-12-27

PRIOR PLING DATE: 2001-12-27

PRIOR PLING DATE: 2001-12-27

PRIOR PLING DATE: 2001-12-26

PRIOR PLING DATE: 2010-10-2-16

PRIOR PLING DATE: 2010-10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 36.2%; Score 50; DB 15; Length 458; Best Local Similarity 40.9%; Pred. No. 1e+02; Matches 9; Conservative 6; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:

CTHER INFORMATION: Clone ID: PAT_MRT4530_83862C.1.pep

US-10-437-963-187128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          232 HGFGNAKRHVLISLSF---YPAFISP 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HNFG---RHWGLPLSFLLNYPLFLSP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 FGRHWGLPLS -- FLLUYPLFLS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Enterococcus faecalis
US-10-282-122A-57060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  à
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RESULT 15

1;

Gaps

13;

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53 ; Search time 5.88679 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-51 138 1 VHNFGRHWGLPLSFLLNYPLFLSP 24

Title: Perfect score: Sequence: Scoring table:

283416 seqs, 96216763 residues BLOSUM62 Gapop 10.0., Gapext 0.5

Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 1 2 E 4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	2 glycoprotein	glycoprotein	coprotein	d trans	hypothetical prote	probable membrane	pern	hypothetical prote	ical	ical	peru		probable membrane	probable transport	membrane protein y	probable transport	hypothetical prote	apolipoprotein B-1	probable transcrip	transport protein	UDP-MurNAc-pentape	UDP-N-acetylmuramo	hypothetical prote	isoleucine-tRNA li	eucine-tF	ρ	lycoprote	11ycoprotein	pro
	DI E		VGIHE	84742		S1501	AB027	H9815	2 AD3132	AC2	T16	ACO	B70	ABO	F90	F64	C85	AF1	2 JH0101	B46	366	ACS	2 G97611	T23	F64	2 F71823	2 T21884	VGIHE	VGIH	H9019
	Length DB	1449	49	449	51	52	72	17	17	67	96	94	21	17	17	77	77	48	784	34	51	17	77	20	20	20	398	47	447	22
* Query	1	3.5	ω.	σ,	σ,	œ.	۲.	7.	۲.	۲.	5.	ď.	ď.	4.	4.	4.	4.	4.	34.8	4	4.	4.	4.	4.	4.	4.	•	34.1	4,	ë.
	Score	09	9	55	54	•	Η.	51	51	51	49.5	4	48.5	4.8	48	48	48	48	48	47	47	47	47	47	47	47	47	47	47	46.5
Result	No.		8	m	4	'n	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	20

hypothetical prote	hypothetical prote	conserved hypothet	D-alanine-D-alanin	related to UDP N-A	probable exporter	related to trfA pr	brefeldin A-sensit	apolipoprotein B -	apolipoprotein B-1	hypothetical prote	hypothetical prote	hypothetical prote	UDP-N-acetylmuramo	hypothetical prote	hypothetical prote
AF2344	876537	D69049	A99901	T50997	T36377	T51071	A53542	JH0102	LPHUB	F71303	D71301	876894	AI3323	D95393	T31640
7	N	~	~	N	N	N	N	N	Н	N	0	~	N	0	~
153	257	355	356	357	531	728	738	779	4563	92	270	460	481	592	684
33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.3	33.0	33.0	33.0	33.0	33.0	33.0
	46	46	46	46	46	46	46	46	46	5.5	5.5	5.5	5.5	5.5	5.5
46										4	4.	4.	4.	47	4

ALIGNMENTS

RESULT 1 A43573 E2 glycoprotei C;Species: Dor C;Date: Dor C;Date: Dor C;Accession: A R;Wessley, R.D. Adv. Exp. Med. A;Title: Nucle A;Accession: Tor A;Accession: A A;Accession: A A;Accession: A A;Accession: A A;Accession: C;Cycycore A;Accession: C;Cycycore C;Cycycore A;Accession: Tor A;Accession	RASSULT 1 A43573 A44573 A44573 A45874 B44573 B19420protein precursor - porcine transmissible gastroenteritis virus (strain Miller) B19420protein precursor - porcine transmissible gastroenteritis virus C.Species: porcine transmissible gastroenteritis virus C.Species: porcine transmissible gastroenteritis virus C.Species: A0-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004 E.Maccession: A43573 B.Wesley R.D. A.M. Exp. Med. Biol. 276, 301-306, 1990 A.M. Exp. Med. Biol. 276, 301-306, 1993 C.Superfamily: coronavirus E2 glycoprotein F.107-1043/Region: hydrophobic F.107-1043/Region: hydrophobic F.107-1043/Region: hydrophobic F.107-1043/Region: hydrophobic Best Local Similarity 60.0%; Score 60; BB 1; Length 1449; Best Local Similarity 60.0%; Pred. No. 1.3; Andelse 12; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
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30 GNHWNLIETFLLNYSSRLSP 49 S GRHWGLPLSFLLNYPLFLSP 24 g ò

RESULT 2
VGIHFS
E2 glycoprotein precursor - porcine transmissible gastroenteritis virus (strain FS772//
NZALternate names: peplomer glycoprotein; spike glycoprotein
NZALternate names: peplomer glycoprotein; spike glycoprotein
C;Species: porcine transmissible gastroenteritis virus
C;Species: porcine transmissible gastroenteritis virus
C;Species: porcine transmissible gastroenteritis virus
C;Accession: B43489; S11728
N;Mius Res. 18, 71960, 1990
N;Mius Res. 18, 71960, 1990
N;Mitch Res. 18, 71960, 1990
N;Mitch Res. 18, 71960, 1990
N;Mitch Res. 19, 71960, 1990
N;Molecule type: mRNA
N;Reference number: A43489
N;Molecule type: mRNA
N;Residues: 1-1449 cBR1:
N;Cross-references: UNIPROT:P18450; GB:X53128; NID:g61377; PIDN:CAA37285.1; PID:g61379
C;Superfamily: coronavirus E2 glycoprotein
C;Keywords: glycoprotein; transmembrane protein
F;1-16/Domain: signal sequence #status predicted <SIG>

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Gaps

2004

14:55:37

Fri Nov 12

g

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54;
39.1%; Score
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probable membrane protein YPO2266 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0276
C;Accession: AB0276
R;Parkhill, J; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MJID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          probable permease of ABC transporter PA1257 [imported] - Agrobacterium tumefaciens (str C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Species: Agrobacterium tumefaciens
C; Accession: H98155
R; Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A; Title: Genome Sequence of the Plant Pathogen and Blotechnology Agent Agrobacterium tu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Cross-references: UNIPROT: Q04350; GB: M57938; NID: g331157; PIDN: AAA67458.1; PID: g33115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A, Cross-references: UNIPROT: Q8ZEB5; GB: AL590842; PIDN: CAC91070.1; PID: 915980262; GSPDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Shapira, R.; Choi, G.H.; Nuss, D.L.
EMBO J. 10, 731-739, 1991
A;Title: Virus-like genetic organization and expression strategy for a double-stranded
A;Reference number: S15009; MUID:91184117; PMID:2009854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein B - Cryphonectria hypovirus 1
C;Species: Cryphonectria hypovirus 1
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 NFGRHW---GLPLSF------LLNY-----PLFLSP 24
                                                  Indels
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37.3%; Score 51.5; Dl
Best Local Similarity 35.6%; Pred. No. 5.6;
Matches 16; Conservative 1; Mismatches
     Best Local Similarity 40.9%; Pred. No. 3;
Matches 9; Conservative 8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38.0%; Score 52.5; I
llarity 54.2%; Pred. No. 37;
Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                514 VRNTGIH-GLPGDFLSNYPRLPTP 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 VHNFGRHWGLPLSFLLNYPLFLSP 24
                                                                                                                                              4 FGRHWGLPLSFL--LNYPLFLS 23
                                                                                                                                                                                                      FGRKWGARVAWLYWINYPIWMA 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A,Status: preliminary
A,Molecule type: genomic RNA
A,Residues: 1-3165 <EMB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
les 13; Conserv
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A;Molecule type: DNA
A;Residues: 1-372 <KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: S15010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: S15010
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Matches
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C. Species: porcine transmissible gastroenteritis virus
C. Species: porcine transmissible gastroenteritis virus
C. Date: 23-Nov-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
C. Accession: S65881, $44423
R. Chen, C.M.; Cavanagh, D.; Britton, P.
Virus Res. 38, 83-89, 1995
A. Filte: Cloning and sequencing of a 8.4-kb region from the 3'-end of a Taiwanese virule
A. Reference number: 865851
A. Freference number: 865850; MUID:96060227; PMID:8546012
A. Reference number: 865851
A. Reference num
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              c. Species: Listeria monocytogenes
C. Species: Listeria monocytogenes
C. Species: Listeria monocytogenes
C. Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C. Species: Listeria monocytogenes
C. Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C. Accession: AF1079
R.Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
C.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A.Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Teletence number: AB1077; MUID:21537279; PMID:11679669
A.; Reference number: AB1077; MUID:21537279; PMID:11679669
A.; Residues: 1-461 GLA>
A.
F;17-1449/Product: E2 glycoprotein #status predicted <E2G>
F;1027-1043/Region: hydrophobic
F;1087-1041/Domain: transmembrane #status predicted <TMN>
F;26,42,71,94,243,250,285,334,345,362,375,405,449,516,532,554,594,704,725,780,819,834,84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E2 glycoprotein precursor - portion, spike protein NAlternate names: envelope protein, spike protein C.Species: porcine transmissible gastroenteritis virus C.Species: 23-Nov-1994 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004 C.Date: 23-Nov-1994 #sequence_revision 19-Apr-1996
                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
                                                                                                                                                                                                                                                                                  43.5%; Score 60; DB 1; Length 1449; llarity 60.0%; Pred. No. 1.3; Conservative 1; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 1449;
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Pred. No. 6.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GNHWNLIETFLLNYSSRLSP 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5 GRHWGLPLSFLLNYPLFLSP
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Local Similarity 55.0%;
les 11; Conservative 3
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 12; Conserv
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hypothetical protein F52C9.1 - Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: Caenorhabditis elegans
C.Species: 20.8ep-1999 #sequence_revision 20.8ep-1999 #text_change 04-Mar-2000
C.Accession: T16424
B.Favello, T.
Submitted to the EMBL Data Library, November 1995
A.Rocciption: The sequence of C. elegans cosmid F52C9.
A.Reference number: Z18511
A.Reference number: Z18511
A.Residues: T1644
A.Residues: T1644
A.Residues: 1-796 < AVA
A.Residues: 1-796 < AV
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(Species: Yersinia pestis

(Species: Yersinia pestis

(Spacession: AC0133

**Parkhill.

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C;Genetics:
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Pred. No. 18;
1; Mismatches 3; Indels
                                                                                                     Length 467
                                                                                                                                                                                                8; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
35.9%; Score 49.5; DB 2;
Best Local Similarity 44.0%; Pred. No. 25;
Matches 11; Conservative 3; Mismatches 10;
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7
                                                                                                     DB
                                                                                                                                                                                           5; Mismatches
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                                                                                                     37.0%;
32.1%;
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267 GNRWGLPFNFLL 278
                                                                                                     Query Match
Best Local Similarity 32.1
Matches 9; Conservative
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Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: AC0133
A,Status: preliminary
A,Molecule type: DNA
          A;Gene: all1673
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          A;Accession: House, A;Accession: House, A;Accession: House, A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Kesidues: 1-217 <KUR>
A;Cross-references: UNIPROT:Q8U6X6; GB:AE007870; PIDN:AAK88770.1; PID:g15158516; GSPDB:GC;Genetics:
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Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
Nakasas, S. 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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A;Status: preliminary
A;Atatus: preliminary
A;Residues: 1-467 «KUR»
A;Residues: 1-467 «KUR»
A;Cross-references: UNIPROT: CBYWEO; GB:BA000019; PIDN:BAB78039.1; PID:g17135493; GSPDB:G
A;Expertimental source: strain PCC 7120
C;Genetics:
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C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AC2015
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Pred. No. 3.8;
4; Mismatches 2; Indels
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A; Reference number: A97359; MUID: 21608551; PMID: 11743194
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Pred. No. 3.8;
4; Mismatches
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A,Map position: linear chromosome
C,Superfamily: histidine permease protein M
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 57.1%;
Matches 8; Conservative
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46 FGPYWSLPLTFVLD 59
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Score 48; DB 2; Length 417; Pred. No. 21; 1; Mismatches 7; Indels

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A,Molecule type: DNA
A,Residues: 1-417 <BLAT>
A,Cross-references: UNIPROT:P43531; GB:AE000255; GB:U00096; NID:g1787875; PIDN:AAC74668
A,Experimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Escherichia coli
C;Date: 12-Sep.1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Datession: F64915
C;Accession: F64915
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
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C.Keywords: inner membrane; transmembrane protein; transport protein
F:39-55/Domain: transmembrane #status predicted <TML>
F:75-91/Domain: transmembrane #status predicted <TML>
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A, Experimental source: strain O157:H7, substrain RIMD 0509952 C, Genetics:
A, Gene: ECs2302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230 NFRLHWRDRGLPLLFAEGFLLMGSFVTLFNYIGYRLMLSP 269
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                                                                                                                                                                                                   C, Superfamily: probable antibiotic resistance protein yybF
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llarity 35.0%;
Conservative
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                                                                                    C, Accession: B70199
R. Fraser, C. M.; Casjens, S.; Huang, M.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White Br. Fraser, C. M.; Casjens, S.; Huang, M.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White son, J.; Rerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B. Nature 390, 580-586, 1997
A, Authors: Smith, H.O.; Venter, J.C.
A,Authors: Smith, J.O.
A,Authors: Smith, J.O.
A,Authors: Smith, J
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                          13-Peb-1998 #sequence_revision 13-Feb-1998 #text_change 09-Jul-2004
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Pred. No. 36;
4; Mismatches 5;
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les 10; Conservative
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R, Parkhill, J.; Doug
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DB 2; Length 417;

Score 48; DB 2 Pred. No. 21; 1; Mismatches

084012 Versinia pe 082eb5 yersinia pe 08zeb5 yersinia pe 08zeb5 yersinia pe 07cvk4 agrobacteri 08u6x6 agrobacteri 08u5x6 ralsconia s 08ywe0 analsconia s 09yra7 transmissib 07kwx7 dicryosteli Aas38666 dicryoste

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AgCP3645 (Fragment).
Name=agCG97535; ORFNames=ENSANGG0000019047;
Name=agCG97535; ORFNames=ENSANGG0000019047;
Anopheles gambiae etr. PSST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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0601L4;
05-UL-2004 (TrEMBLrel. 27, Created)
05-UL-2004 (TrEMBLrel. 27, Last sequence update)
05-UL-2004 (TrEMBLrel. 27, Last annotation update)
Spike glycoprotein (Fragment).
Transmissible gastroenteritis virus.
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-sfrand viruses, no DNA stage; Nidovirales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        preliminary data.

EMBL; AABA01008807; EAA04057.1; -.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0005279; F:amino acid-polyamine transporter activity; IEA.

GO; GO:0006865; P:amino acid transport; IEA.

InterPro; IPR002422; AA/rel_permease2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-PEST;
Anotheles Genome Sequencing Consortium;
Anotheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/Genbank/DDBJ databases.
-- CAUTION: The sequence shown here is derived from an EMBL/Genbank/DDBJ whole genome shotgun (WGS) entry which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45.7%; Score 63; DB 2; Length 475;
45.0%; Pred. No. 1.5;
tive 6; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 26, Created)
(TrEMBLrel. 26, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                     475 AA
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07TQN3
09YTU2
09YTU2
08YTU2
08D0135
08EB5
08BWE9
07CVK4
08UGX6
08UGX6
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AAS38666
Q8VGY6
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les 9; Conservative
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN=HN2002;
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O9ywn8 banna virus
Aas68264 colliviru
Aas68265 colliviru
Q85085 transmiseib
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                                                                                                      November 10, 2004, 13:38:57; Search time 31.9698 Seconds (without alignments) 431.938 Million cell updates/sec
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O41204
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               GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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1 VHNFGRHWGLPLSFLLNYPLFLSP 24
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070352
AAS68178
VGL2_CVPFS
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06F055
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080R80
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Maximum Match 100%
Listing first 45 summaries
                                                                           - protein search, using sw model
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1: uniprot_sprot:*
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-!- SUBCELLULAR LOCATION: Type I membrane protein.
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01-FEB-1996 (
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VGL2 CVPMI
ID VGL2 CVPMI
AC P33470;
DT 01-FEB-1994
DT 01-FEB-1996
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MEDLINE=91188699; PubMed=1964522;
Britton P., Page K.W.;
Sequence of the S gene from a virulent British field isolate of
"Sequence of the S gene from ";
Virus Res. 18:71-80(1990).
-!- FUNCTION: The peplomer protein mediates the binding of virions to
the host cell receptor and is involved in membrane fusion and in
syncytium formation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=HW3002;
He K., Ni Y.;
"Transmissible gastroenteritis virus strain HW2002 spike glycoprotein
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(TGEV).
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29-MRA-2004 (TrEMBLrel. 27, Last sequence update)
29-MRA-2004 (TrEMBLrel. 27, Last annotation update)
59-MRA-2004 (TrEMBLrel. 27, Last annotation update)
Spike glycoprotein (Fragment).
Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; coronavirus; Group I species.
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Coronaviridae; Coronavirus.
NCBI_TaxID=11150;
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01-NOV-1990 (Rel. 16, Created)
01-ARR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein).
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43.5%; Score 60; DB 2; Length 269;
Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 12; Conservative 1; Mismatches 7; Indels
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Best Local Similarity 60.0%; Pred. No. 2.4;
Matches 12; Conservative 1; Mismatches 7; Indels
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Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS39716; AAS68178.1; -.
      He K., Ni Y.;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AX539716; AAS68178.1; -.
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AAS68178
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement, (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                      E2 glycoprotein.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
                                                                                                              EMBL; X53128; CAA37285.1; -.
PIR; B43489; VGIHFS.
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S2.
Pfam; PF01600; Corona_S1; 1.
Pfam; PF01601; Corona_S2; 1.
Envelope protein; Glycoprotein; Signal; Transmembrane.
SIGNAL
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Pred. No. 13;
1; Mismatches
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(Rel. 33, Last sequence update)
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CARBOHYD
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 "Nucleotide sequence of the E2-peplomer protein gene and partial nucleotide sequence of the upstream polymerase gene of transmissible gas gastroenteritis virus (Miller strain).";
Adv. Exp. Med. Biol. 276:301-306(1990).
-!- FUNCTION: The peplomer protein mediates the binding of virions to the host cell receptor and is involved in membrane fusion and in
05-JUL-2004 (Rel. 44, Last annotation update)
E2 glycoprotein precursor (Spike glycoprotein) (Peplomer protein).
Name=S;
                                                                                 Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus
                                                 Porcine transmissible gastroenteritis coronavirus (strain Miller)
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By glycoprotein.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Cys.rich.
N-linked (GlcNAc. . ) (Pote
                                                                                                                                                                                                                                                                                                    syncytium formation.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
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N-linked
N-linked
                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=91353366; PubMed=1966416;
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                                                                                                                 NCBI_TaxID=33737;
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Gaps
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G6PQ05;
G5-UDL-2004 (TrEMBLrel. 27, Created)
G5-UJL-2004 (TrEMBLrel. 27, Last sequence update)
G5-UJL-2004 (TrEMBLrel. 27, Last annotation update)
Spike glycoprotein.
Transmissible gastroenteritis virus.
Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus; Group 1 species.
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Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group I species.
N-linked (GlCNAC. ..) (Potential)
N-linked (GLCNAC. ..) (Potential)
N-linked (GLCNAC. ..) (Potential)
MW; FFC3CB8AAC9FB655 CRC64;
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                                                                                        DB 1; Length 1449;
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He K., Yang Q.;

Bubmitted (ARR-2004) to the EMBL/GenBank/DDBJ databases.

BMBL; AYS888822; AAT00645.1; -.

InterPro; IPR002551; Corona_S1.

InterPro; IPR002552; Corona_S2.

Pfam; PF01600; Corona_S1; 1.

Pfam; PF01601; Corona_S1; 1.

SEQUENCE 1449 AA; I59953 MW; 237E61F2373933A1 CRC64;
                                                                                                                               7; Indels
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                                                                                                                             1; Mismatches
                                                                                           Score 60;
Pred. No.
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 1341 1341
1358 1358
1371 1371
1449 AA; 159916 M
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Best Local Similarity 60.07
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                                                                                                             Local Similarity
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no DNA stage; Nidovirales;

Last sequence update) Last annotation update)

Created)

184 AA.

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"Restriction mapping of genome and nucleotide sequence of Aujeszky's disease virus strains isolated in CIS."; Vopr. Virusol. 44:254-257(1999).

NON. TER 184 184 184 SEQÜENCE 184 AA; 21010 MW; 31E308C3B21D76D2 CRC64;
                                                                                                                                                                                                                                                                 STRAIN=TMK-22;
MEDLINE-20128444; PubMed=10665059;
Aminev A.G., Amineva S.P., Baborenko E.F., Mishchenko V.A.,
                                                                                                                                                                Transmissible gastroenteritis virus.
Viruses, ssRNA positive-strand viruses, no Di
Coronaviridae, Coronavirus, Group I species.
NCBI_TaxID=11149;
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55.0%; Pred. No. e..,
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                                                                           ol-JAN-1998 (TrEMBLrel. 05, C. 01-JAN-1998 (TrEMBLrel. 05, Lt. 01-DEC-2001 (TrEMBLrel. 19, Le Glycoprotein S (Fragment).
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Best Local Similarity 55.0%
Matches 11; Conservative
                                                                PRELIMINARY;
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                  Gaps
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"The S gene of cannine coronavirus, strain UCD-1, is more closely
related to the S gene of transmissible gastroenteritis virus than to
that of feline infectious peritonitis virus.";
Virus Res. 61:145-152(1999).
EMBL, AF116248; AAA4990'.1; -.
InterPro; IPR002551; Corona_S1.
InterPro; IPR002552; Corona_S1.
Pfem, PF01600; Corona_S2.
Pfem, PF01601; Corona_S2; 1.
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Transmishible gastroenteritis virus.
Viruses; sSRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Gronavirus; Group 1 species.
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Coronaviridae; Coronavirus; Group 1 species.
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Pred. No. 13;
1; Mismatches 7; Indels
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                                                                                                                                                                                                                                                                                                                                             STRAIN=HN2002;
He K., Yang Q.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS68882; AAT00645.1; -.
SEQUENCE 1449 AA; 159953 MW; 237E61F2373933A1 CRC64;
                  7; Indels
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                                                                                                                                                                        AATO0645;
10-MAY-2004 (TrEMBLrel. 27, Created)
10-WAY-2004 (TrEMBLrel. 27, Last sequence update)
10-WAY-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-DBC-2001 (TrEMBLrel. 19, Last annotation update)
S protein (Fragment).
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 60.0%; Pred. No. 13;
tive 1; Mismatches
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MEDLINE=99402069; PubMed=10475084;
                                               5 GRHWGLPLSFLLNYPLFLSP 24
                                                                           30 GNHWNLIETFLLNYSSRLSP 49
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Best Local Similarity 60.0%;
Matches 12; Conservative
                  12; Conservative
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Best Local Similarity
Matches 12; Conserv
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Gaps

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8; Indels

Score 55; DB 2; Length 184; Pred. No. 8.4;

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Coronaviridae; Coronavirus; Group 1 species.
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MEDLINE=22699991; PubMed=12814887;
MEDLINE=22699991; PubMed=12814887;
Kim S.J., Han J.H., Kwon H.M.;
Kim S.J., Han J.H., Kwon H.M.;
Reatial sequence of the spike glycoprotein gene of transmissible gastroenteritis viruses isolated in Korea.";
Ver. Microbiol. 94:195-206(2003).
Ver. Microbiol. 94:195-206(2003).
InterPro; IPRO02551; Corona S.I.
Pfam; PF01600; Corona S.I.
NON TER 789 789
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                                                   01-UN-2002 (TrEMBLrel. 21, Created)
01-UN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Spike glycoprotein (Fragment).
Transmissible gastroenteritis virus.
789 AA.
PRT;
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RESULT 12

30 GNHWNLIENFLLNYSIRLPP 49

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Coronaviridae; Coronavirus; Group 1 species.
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       SET REPRESENTATION OF THE PROPERTY OF THE PROP
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group 1 species.
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Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
                                                                           Q8QRR9;
Q8QRR9;
01-UUN-2002 (TrEMBLrel. 21, Created)
01-UUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
Spike glycoprotein (Fragment).
Spike glycoprotein (Fragment).
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group 1 species.
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llarity 55.0%; Pred. No. 36;
Conservative 1; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
39.9%; Score 55; DB 2; Length 789;
Best Local Similarity 55.0%; Pred. No. 36;
Matches 11; Conservative 1; Mismatches 8; Indels
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STRAIN=KT5;
Kim S.J., Kwon H.M.;
Kim S.J., Kwon H.M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AF481363; AAL89742.1; -.
InterPro; IPR002251; Corona_S1.
Pfam; PF01600; Corona_S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=KT6;
Kim S.J., Kwon H.M.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBU databases.
EMBL; AF481364; AAL89743.1; -.
InterPro; IPR002251; Corona_S1.
Pfam; PF01600; Corona_S1;
NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 789 AA; 87647 MW; 17F00DB0BEB992BB CRC64;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
                                                 789 AA
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ses 11; Conserv
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QBQRS3;
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                                                    Q8QRR9
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Matches
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Q8QRS0
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Transmissible gastroenteritis virus.
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus; Group 1 species.
                                                                                                            Kim S.J., Han J.H., Kwon H.M.;
Partial sequence of the spike glycoprotein gene of transmissible
gastroenteritis viruses isolated in Korea.";
Vet. Microbiol. 94:195-206(2003).
EMBL, AF481360; AAL89739.1;
PinterPro; IPR002551; Corona_S1.
Pfam: PF0100_Corona_S1.
NON_TER 789 789
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"Partial sequence of the spike glycoprotein gene of transmissible agatroenteritis viruses isolated in Korea.";
Vet. Microbiol. 94:192-206(2003).
EMBL, AF481361; AAL89740.1;
PinterPro; IPR002551; Corona. S1.
Pfam; PF00000 Corona. S1.
Pfam; PF00000 Corona. S1.
Pfam; PF00000 Corona. S1.
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                                                                                                                                                                                                                                                                                                                                    Length 789;
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789 AA; 87600 MW; 615882B621F24FF2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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39.9%; Score 55; DB 2;
Best Local Similarity 55.0%; Pred. No. 36;
Matches 11; Conservative 1; Mismatches
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MEDLINE=22699991; PubMed=12814887;
                                                                                      MEDLINE=2269991; PubMed=12814887;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               | || | :||||| | 30 GNHWNLIETFLLNYSSRLPP 49
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Best Local Similarity 55.03
Matches 11; Conservative
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                                       SEQUENCE FROM N.A.
NCBI_TaxID=11149;
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01-JUN-2002
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US-09-299-495F-11
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Sequence 11, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 18, Appl
Sequence 28902, A
Sequence 28902, A
Sequence 28902, A
Sequence 487, Appl
Sequence 4, Appli
Sequence 4, Appli
Sequence 2, Appli
                                                               November 10, 2004, 13:44:14; Search time 14.6415 Seconds (without alignments) 181.178 Million cell updates/sec
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Sequence
Sequence
                                                                                                           US-10-092-750-52
194
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2: /cgn2 6/ptodata/1/laa/5B_COMB.pep:*
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6: /cgn2 6/ptodata/1/laa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-690-011A-11

US-08-690-011A-11

US-09-134-06447

US-09-344-624-12

US-09-344-624-12

US-09-344-624-12

US-09-344-86-88

US-09-324-86-88

US-10-320-18

US-09-328-352-8902

US-09-328-352-7488

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US-08-585-758A-2

US-08-585-758A-2

US-08-585-758A-2

US-08-178-187-2

US-08-178-187-2

US-08-146-187-2

US-08-146-187-3

US-09-146-187-3
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                                                                                                                                                                                     478139 seqs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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                                           protein search, using
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                            OM protein
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                                                                                                                                                                                         Searched:
                                                                   Run on:
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APPLICANT: VINSON, Charles R.
APPLICANT: VINSON, Dmitry
TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF CELLULAR PROTEIN
           Sequence 1, Appli
Sequence 2, Appli
Sequence 478, Appli
Sequence 478, App
Sequence 5057, Ap
Sequence 5057, Ap
Sequence 3, Appli
Sequence 47583, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: USA

ZIPE: 10154-0053

COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC Compatible
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/299,495F
FILING DATE: 26-Apr-1999
PRIOR APPLICATION NUMBER: G0/001,654
FILING DATE: 31-JUL-1995
APPLICATION NUMBER: G0/018,496
FILING DATE: 32-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 208(690,011
FILING DATE: 31-JULY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Serunian, Leslie A.
REGISTRATION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 2026-4199USZ
TELEPHONE: (212)758-4800
TELEPAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 11:
SEGUREACTER. AS A sin no acids
US-08-786-999-1

US-09-216-3187-1

US-09-886-31387-1

US-09-886-3198-1

US-09-604-2188-478

US-09-604-2878-478

US-09-604-2878-478

US-09-604-2878-485

US-09-834-759-485

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US-09-834-759-485

US-09-834-759-485

US-09-131-999C-6463

US-09-131-999C-6463

US-09-131-999C-6463

US-09-270-674-3

US-09-270-674-3

US-09-270-674-3

US-09-270-674-3

US-09-270-674-3
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/09299495F
Patent No. 6361968
GENERAL INFORMATION:
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NO: 11:

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us-10-092-750-52.rai

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US-09-344-624-12; Sequence 12, Application US/09344624; Patent No. 6753154; GENERAL INFORMATION:
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                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.4%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                      US-09-134-000C-4847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-513-999C-5543
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LENGTH: 97
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EXTENSION OF A PROTEIN-PROTEIN
EXTENSION OF A PROTEIN ON SURFACE TO INACTIVATE THE FUNCTION OF A CELLULAR PROTEIN
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      DB 3; Length 84;
                                                13; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: NY
COUNTRY: NY
COUNTRY: USA
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: FORDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,011A
FILING DATE: 31-UUL-1996
PRIOR APPLICATION DATA: 60/001,654
FILING DATE: 31-UUL-1995
PRIOR APPLICATION DATA: 31-UUL-1996
ATTORNEY/AGENT: INFORMATION:
NAME: Serunian, Leslie A.
RESISTRAION NUMBER: 35,353
REFERENCE/DOCKET NUMBER: 35,354
REPERENCE/COCKET NUMBER: 35,354
REPERENCE/COCKET NUMBER: 35,355
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION NUMBER: 35,354
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
                                                                                                                 33 LARENEELEKEAEELEQELAELENRVAVLENQNKT 67
                                                                                        6 VGRDAETLOKOKETIKAFLKKLEALMASNDNANKT
Query Match 29.4%; Score 57; DB 3
Best Local Similarity 37.1%; Pred. No. 2.7;
Matches 13; Conservative 9; Mismatches
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                                                                                                                                                                                                                                   Sequence 11, Application US/08690011A
Patent No. 5942433
GENERAL INFORMATION:
APPLICANT: VINSON, Charles R.
APPLICANT: KRYLOV, DMILTY
TITLE OF INVENTION: EXTENSION OF A PROTEI
TITLE OF INVENTION: ELLULAR PROTEIN
TITLE OF INVENTION: CELLULAR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CONTY: NOW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 37.1
Matches 13; Conservative
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MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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US-09-134-000C-4847

Sequence 4847, Application US/09134000C

Patent No. 6617156

GRNERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

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| Sequence 5434, Application US/09513999C
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Duclert, A.:
| APPLICANT: Duclert, A.:
| TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
| PATENT FILE REFRENCE: 59.USZ.REG
| CURRENT FILING DATE: 2000-02-24
| PRIOR PPLICATION NUMBER: US 60/122,487
| PRIOR PLILING DATE: 1999-02-26
| NUMBER OF SEQ ID NOS: 36681
| SOFTWARE: Patentt.pm
| SRO Th No. 6442
ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
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APPLICANT: Chen, Hues-Mei
APPLICANT: Chen, Hues-Mei
APPLICANT: Bissell, Mina
TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
TITLE OF INVENTION: HUMAN AZ-1 GENE, VARIANTS THEREOF AND EXPRESSED GENE
FILE REFERENCE: 2960-44(HV)
CURRENT APPLICATION NUMBER: US/09/344,624
CURRENT FILING DATE: 1999-06-25
EARLIER FILING DATE: 1998-06-26
EARLIER FILING DATE: 1998-06-26
SOFTWARE: PATENTION VOIC: 2.0
SOFTWARE: PATENTIN VET: 2.0
SEQ ID NO 12
LENGTH: 223
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22;
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Pred. No. 22;
7; Mismatches
                 FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFWARE: Patentin version 3.1
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23 QVIARSRETRAAYLKRIEAAIAEGPQRNK 51

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| Patent No. 676//44
| GENERAL INFORMATION:
| APPLICANT: Coffas, Martin
| APPLICANT: Coffas, Martin
| APPLICANT: Coffas, Martin
| APPLICANT: OGOM, J. Martin
| APPLICANT: No. 6767744ton, Kelley C.
| APPLICANT: No. 6767744ton, Kelley C.
| TITLE OF INVENTION DEMITRIPYING METHANOTROPHIC BACTERIAL STRAIN
| TITLE OF INVENTION DEMITRIPYING METHANOTROPHIC BACTERIAL
| TITLE OF INVENTION NUMBER: US/10/321,210
| CURRENT APPLICATION NUMBER: US/09/934,901
| PRIOR PILING DATE: 2001-08-22
| PRIOR PILING DATE: SOUGH-08-22
| PRIOR FILING DATE: September 1, 2000
| SOFTWARE: Microsoft Office 97
| SEQ ID NO 18
| LENGTH: 618
| LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | FAUERIA INCORMATION:
| APPLICANT: KOffas, Mattheos
| APPLICANT: Odom, J. Martin
| APPLICANT: Odom, J. Martin
| APPLICANT: No. 671305con, Kelley C.
| APPLICANT: Ye, Rick
| APPLICANT: Ye, Rick
| TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
| TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
| FILE REFERENCE: CLIG.9 US NA
| CURRENT FILING DATE: 2002-12-17
| PRIOR PPLICATION NUMBER: US/09/934,901
| PRIOR PPLICATION NUMBER: 60/229,906
| PRIOR FILING DATE: September 1, 2000
| NUMBER OF SEQ ID NOS: 20
| NUMBER OF SEQ ID NOS: 20
| SOFFWARE: Microsoft Office 97
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28.4%; Score 55; DB 4; Length 618;
Best Local Similarity 34.5%; Pred. No. 44;
Matches 10; Conservative 8; Mismatches 11; Indels
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Pred. No. 44;
8; Mismatches 11; Indels
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                                                              RESULT 8
US-10-321-210-18
i Sequence 18, Application US/10321210
sequence 18, Application US/10321210
patent No. 6767744
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; Patent No. 6773905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 34.5%;
Matches 10; Conservative
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ORGANISM: METHYLOMONAS SP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-252-991A-28902
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; Sequence 8, Application US/09934868
; Sequence 8 Application US/09934868
; Patent No. 6689601
; GENERAL INFORMATION:
; APPLICANT: ADGOM, James M
; APPLICANT: Schenzle, Andreas J
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFREENCE: CL1556 US NO.
; TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
; FILE REFREENCE: C1056 US NO.
; FILE PREFREENCE: C1050 US NO.
; FILE PREFREENCE: C001-08-22
; PRIOR FILING DATE: 2001-08-22
; PRIOR FILING DATE: 2001-09-01
; NUMBER OF SEQ ID NOS: 81
; SOFFWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                           US-00-934-901-18
Sequence 18, Application US/09934901
Sequence 18, Application US/09934901
Sequence 18, Application US/09934901
Sequence 18, Application
Sequence 18, Application
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Matthin
APPLICANT: No. 655535ton, Kelley C.
APPLICANT: No. 655535ton, Kelley C.
APPLICANT: No. 655535ton, US/09/0914
TITLE OF INVENTION: DENTERPYING METHANOTROPHIC BACTERIAL STRAIN
FILE REPERENCE: CL1619 US NA
CURRENT APPLICATION NUMBER: 60/229, 906
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NOS: 20
SEQ ID NOS: 20
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28.4%; Score 55; DB 4; Length 618;
Best Local Similarity 34.5%; Pred. No. 44;
Matches 10; Conservative 8; Mismatches 11; Indels
                                                                                               Query Match
28.4%; Score 55; DB 4; Length 223;
Best Local Similarity 42.1%; Pred. No. 14;
Matches 16; Conservative 5; Mismatches 11; Indels
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8; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 55;
Pred. No.
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28.4%;
Best Local Similarity 34.5%;
Matches 10; Conservative
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ORGANISM: METHYLOMONAS SP.
US-09-934-901-18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-624-12
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GENERAL INC. 802703
GENERAL INC. 802703
GENERAL INC. 802703
GENERAL INC. 802703
APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI.
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.1002-001
CURRENT PILING NUMBER: US 60/543,681A
CURRENT FILING DATE: 2000-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
BRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 7696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Jiang, Yuqiu
APPLICANT: Jiang, Yuqiu
APPLICANT: Dillon, Davin C.
APPLICANT: Micchan, Jennifer i.
APPLICANT: Micchan, Jennifer i.
APPLICANT: Mulliam I.
APPLICANT: Harlocker, Susan I.
APPLICANT: Hepler, William I.
TITLE OF INVENTION: COMPOSITION:
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT APPLICATION NUMBER: US/09/620,405B
CURRENT FILING DATE: 2000-07-20
NUMBER OF SEQ ID NOS: 495
SOFTWARE: FastsEQ for Windows Version 3.0
SEQ ID NO 487
LENGTH: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1086;
                               Score 53; DB 4; Length 263;
Pred. No. 31;
3; Mismatches 13; Indels
                                                                                                                                                                               5; Mismatches 15; Indels
                                                                                                                                                6 VGRDA----BTLQKQKETIKAFLKKLEALMASND----NAN 38
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Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                        US-09-543-681A-7696
; Sequence 7696, Application US/09543681A
; Patent No. 6605709
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                                  Query Match
Best Local Similarity 39.5%;
Matches 17; Conservative
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Best Local Similarity 38.2%;
Matches 13; Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) ORGANISM: Proteus mirabilis
US-09-543-681A-7696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.1:
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
US-09-620-405B-487
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Patent No. 6562958
GENERAL INFORMATION:
FOR THE SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GT-99-03P8
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF EM 1999-06-04
NUMBER OF SEQ ID NOS: 8252
LENGTH: 232
                                                            APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 28902
LENGTH: 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7488, Application US/09328352

Patent No. 6562958

Patent No. 6562958

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: BUUCHBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER TITLE OF INVENTION: BUUCHBIC ACID AND THERAPEUTICS

FILE OF INVENTION: BUUCHBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER FILE REPRENCE: GTC99-03PA

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 7488
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27.8%; Score 54; DB 4; Length 373;
Best Local Similarity 36.4%; Pred. No. 34;
Matches 12; Conservative 9; Mismatches 12; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ASMAPVGRDAETLOKOKETIKAFLKKLEALMAS 33
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Sequence 28902, Application US/09252991A Patent No. 6551795
Battent INFRMATION: APPLICANT: APPLICANT: MARC J. Rubenfield et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-7488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Acinetobacter baumannii
US-09-328-352-8025
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-28902
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US-09-328-352-8025
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US-09-328-352-7488
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Gaps

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Score 52; DB 4; Length 235; Pred. No. 37; 6; Mismatches 15; Indels
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us-10-092-750-52.rai
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Sequence 18, Appl Sequence 18, Appl Sequence 166, App Sequence 6510, Ap Sequence 6510, Ap Sequence 510, Ap Sequence 19923, Sequence 19923, Sequence 19923, Sequence 19923, Sequence 19035, Sequence 100351, Sequence 100351, Sequence 110351, Sequence 2287, Sequence 2287, Sequence 2287, Sequence 2287, Sequence 217430, Sequence 217430, Sequence 217430, Sequence 217430,

Perfect score:

Run on:

Sequence:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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Length 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 52, Application US/10092750

Sequence 52, Application No. US2033003157A1

GENERAL INFORMATION:

APPLICANT: Hammond, Philip W.

APPLICANT: Hammond, Philip W.

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REFERENCE: 50036/050002

CURRENT PILING DATE: 2002-03-07

PRIOR FILING DATE: 2001-03-08

NUMBER OF SEQ ID NOS: 253

SEQ ID NO 52

LENGTH: 40

LENGTH: 40
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                     US-10-220-924-18

US-10-320-874-18

US-10-320-874-18

US-10-320-874-18

US-10-320-874-166

US-10-369-493-6146

US-10-369-493-6510

US-10-369-493-6510

US-10-424-599-199232

US-10-425-114-36706

US-10-425-114-64315

US-10-425-115-190351

US-10-282-122A-61644

US-10-282-122A-61644

US-10-282-122A-61644

US-10-283-1234

US-10-283-329-143

US-10-283-329-143

US-10-283-329-143

US-10-283-329-143

US-10-283-329-143

US-10-283-329-143

US-10-283-329-144

US-10-283-329-144

US-10-283-329-144

US-10-283-329-144

US-10-177-293-123

US-10-177-293-123

US-10-177-293-123

US-10-425-115-205253

US-10-425-115-205253

US-10-425-115-205253

US-10-117-293-123

US-10-117-293-133

US-10-425-115-205253

US-10-425-115-205253

US-10-425-115-207-64
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100.0%; Pred. No. 5e-18;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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US-09-886-535-4
; Sequence 4, Application US/09885535
; Patent No. US20020104105A1
; GENERAL INFORMATION:
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40; Conservative
                                                                                                                                                                                                           TYPE: PRT
, ORGANISM: Homo sapiens
US-10-092-750-52
RESULT 1
US-10-092-750-52
Query Match
Best Local S:
Matches 40
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Sequence 4, Appli
Sequence 1911, Ap
Sequence 31994, A
Sequence 3996, Ap
Sequence 741, App
Sequence 47358, A
Sequence 52947, A
Sequence 11, Appl
Sequence 11, Appl
Sequence 126832,
Sequence 11, Appl
                                                                                      November 11, 2004, 01:28:30; Search time 46.2642 Seconds (without alignments) 305.399 Million cell updates/sec
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| Ggn2_6/ptodata//pubpaa/US07_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US06_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US06_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US06_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US06_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US08_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US08_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US08_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US08_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US09A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US106_PUBCCMB.pep:*
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| Ggn2_6/ptodata//pubpaa/US106_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US10F_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US10A_PUBCCMB.pep:*
| Ggn2_6/ptodata//pubpaa/US11_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US11_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US11_NEW_PUB.pep:*
| Ggn2_6/ptodata//pubpaa/US11_NEW_PUB.pep:*
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1 ASMAPVGRDAETLQKQKETIKAFLKKLEALMASNDNANKT 40
              GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-09-885-535-4

6 US-10-408-75A-2687

4 US-10-094-749-1911

4 US-10-094-749-1911

4 US-10-029-386-33994

5 US-10-408-765A-741

5 US-10-282-122A-47358

1 US-10-282-122A-52947

1 US-10-282-122A-52947

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Maximum Match 1008
Listing first 45 summaries
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Sequence 2687, Application US/10408765A

Publication No. US20040101874A1

GENERAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Tahy, Baing

APPLICANT: Tahay, Baing

APPLICANT: Taylor, Steven W.

APPLICANT: Glenn, Gary M.

APPLICANT: Glenn, Gary M.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REPRESENCE: 660088 465

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: PASKSEQ for Windows Version 4.0

SEQ ID NO 2687

LENGTH: 5771
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APPLICANT: Myriad Genetics, Inc.,
APPLICANT: Heichman, Karen,
TITLE Bartel, Paul L.,
TITLE BOLIVENTION: Protein-Protein Interactions;
FILE REPRENCE: 2318-266-II
CURRENT APPLICATION NUMBER: US/09/885,535
CURRENT PILING DATE: 2001-06-21
PRIOR FILING DATE: 2000-06-22
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 2835
                                                                                                                                                                                                                                                                                                                                                                                         Query Match 97.9%; Score 190; DB 9; L
Best Local Similarity 100.0%; Pred. No. 2.1e-15;
Matches 39; Conservative 0; Mismatches 0;
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97.9%; Score 190; DB 16;
Best Local Similarity 100.0%; Pred. No. 4.3e-15;
Matches 39; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; LOCATION: 4471
; OTHER INFORMATION: Xaa = Any Amino Acid
US-10-408-765A-2687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1911, Application US/10094749
Publication No. US20030219741A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: ISOGAI, TAKAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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US-10-094-749-1911
                                                                                                                                                                                                                                                                                                                                               US-09-885-535-4
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SUGIYAMA, TOMOYASU OTSUKI, TETSUJI WAKAMATSU, AI

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Sequence 33994, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICAMT: Penn, Sharron G.
APPLICAMT: Rank, David R.
APPLICAMT: Rank, David R.
APPLICAMT: Rank, David R.
APPLICAMT: HAnzel, David R.
APPLICAMT: REALK, David R.
APPLICAMT: REPERSION HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: EXPRESSION ANALYSIS TWO FILE REFERENCE: AECMICA-X-2 CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT PILING DATE: 200112-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33994
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CTHER INFORMATION: MAP TO AL137853.3
CTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.3
CTHER INFORMATION: SWISSPROT HIT: QSUPN3, EVALUE 0.00e+00
US-10-029-386-33994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 186; DB 14;
Pred. No. 2.6e-15;
1; Mismatches 0;
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                                                                                                                                                                                                    APPLICANT: SORIL, MACHINO
APPLICANT: YOSHIKWA, TSUTOMU
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: OTSUKA, MOTOYUKI
APPLICANT: MASCHALI, KENUI
APPLICANT: MASUHO, YASCHIKO
TITLE OF INVENTION: NOVEL FULL-LENGTH CDNA
FILE REFERENCE: 064325/0160
CURRENT APPLICATION NUMBER: US/10/094,749
CURRENT APPLICATION NUMBER: G0/350,435
PRIOR APPLICATION NUMBER: G1/350,435
PRIOR FILING DATE: 2002-03-12
PRIOR FILING DATE: 2001-09-14
PRIOR FILING DATE: 201-09-14
NUMBER: OF SEQ ID NOS: 3381
SQ ID NO 1911
LENGTH: 1174
TYPE: PRT
CREANISM: Homo sapiens
US-10-094-749-1911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 363 MGAIGRDTDSLQSQIEDVRLFLNKIHVL 390
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ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 97.4%;
Matches 38; Conservative
                                                                                                                                                                 TAMECHIKA, ICHIRO SEKI, NAOHIKO
                                                                    HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                             IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 12; Conservat
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: ELITRA.034
FILE REPERENCE: ELITRA.034
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRIOR APPLICATION NUMBER: 60/194,078
FRIOR APPLICATION NUMBER: 60/206,848
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-23
FRIOR PELING DATE: 2000-05-66
FRIOR PELING DATE: 2000-05-66
FRIOR PELING DATE: 2000-05-66
FRIOR PELING DATE: 2000-03-66
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-10-23
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-11-27
FRIOR PELING DATE: 2000-11-27
FRIOR APPLICATION NUMBER: 60/267,636
FRIOR PELING DATE: 2000-12-22
FRIOR PELING DATE: 2000-12-22
FRIOR PELING DATE: 2000-12-22
FRIOR PELING DATE: 2000-12-22
FRIOR PELING DATE: 2001-02-09
FRIOR FILING DATE: 2001-03-04
FRIOR FILING DATE: 2001-03-04
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FRIOR FILING DATE: 2001-03-04
FRIOR
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APPLICANT: Yanamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms FILE REFERENCE: ELITRA, 034A
CURRENT PAPLICATION NUMBER: 00/10/282,122A
CURRENT FILING DATE: 2003-220
PRIOR APPLICATION NUMBER: 60/10-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 15; Length 174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PVGRDAETLOKOKETIK---AFLKKLEALMASNDNANK 39
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Best Local Similarity 42.1%; Pred. No. 3.9;
Matches 16; Conservative 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            , Sequence 52947, Application US/10282122A ; Publication No. US/20040029129A1
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APPLICATION WUMBER: 60/191,078
ELING DATE: 2000-03-21
APPLICATION NUMBER: 60/206,848
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APPLICATION NUMBER: 60/207,727
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APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohlsen, Kari
Zyskind, Judith
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                                                                                                                                                                                       APPLICANT: Zhang, Bing
APPLICANT: Glason, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Warnock, Dale E.
TITLE OF INVENTION: TAKETS FOR THERAPEUTIC INTERVENTION
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 3896, Application US/10108260A; Publication No US2004005560A1; GENERAL INCORPATION:
; APPLICANT: HELIX RESEARCH INSTITUTE; TITLE OF INVENTION: No. US20040005560A1e; FILE REFREENCE: H. A0106; CURRENT APPLICATION NMBER: US/10/108,260A; CURRENT FILING DATE: 2002-03-27; NUMBER OF SEQ ID NOS: 5458; SOFTWARE: PatentIn Ver. 2.1; SEQ ID NO 3.896; LENGTH: 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 15; Length 990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3027 MGAIGRDIDSLQSQIEDVRLFLNKHVL 3054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            713 ASMSPIGTDLETVKQQIEELKQF--KSEA 739
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Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Sysind, Judith
APPLICANT: Zysind, Judith
APPLICANT: Wall, Daniel
                        Sequence 741, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Eoin D.
APPLICANT: Zhang, Bing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-408-765A-741
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; ORGANISM: Homo sapiens
US-10-108-260A-3896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-282-122A-47358
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LENGTH: 5373
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Gaps

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US-10-425-115-351517

US-10-425-115-351517

Sequence 351517, Application US/10425115

Publication No. US20040214272A1

GREBRAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: APPLICANT: Thou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: 136-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 351517

LENGTH: 217
    APPLICANT: VINSON, Charles K.
APPLICANT: VINSON, Charles K.
TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN
INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A
CELLULAR PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:

NAME: SCHULLAN, Lebelle A.

REGISTRATION NUMBER: 35,353

REFERENCE/DOCKET NUMBER: 2026-4199US2

TELECOMUNICATION INFORMATION:

TELEPHONE: (212)756-4800

TELEFAX: (212)751-6849

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 84 aming acids
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29.4%; Score 57; DB 14;
Best Local Similarity 37.1%; Pred. NO. 8.9;
Matches 13; Conservative 9; Mismatches 13
                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 VGRDAETLOKOKETIKAFLKKLEALMASNDNANKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/059,720
PLING DATE: 29-Jan-2002
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/001,654
FILING DATE: 31-JUL-1995
APPLICATION NUMBER: 60/018,496
APPLICATION NUMBER: 60/018,496
APPLICATION NUMBER: 08/690,011
FILING DATE: 31-JULY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS WORD 97
SOFTWARE: ASCII
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COUNTRY: USA
              GENERAL INFORMATION
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Publication No. US20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Rovalic, David K.
APPLICANT: APPLICANT: AND APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: APPLICANT: David K.
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PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-09
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-10-23
PRIOR PELING DATE: 2000-11-27
PRIOR PELING DATE: 2000-11-27
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PRIOR PELING DATE: 2000-12-27
PRIOR PELING DATE: 2000-12-22
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2001-02-09
PRIOR PELING DATE: 2001-02-06
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-02-16
PRIOR PELING DATE: 2010-02-16
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PELING DATE: 2010-02-16
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US-10-425-115-236832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 32.2%; Score 62.5; DB 15; Best Local Similarity 50.0%; Pred. No. 8.4; Matches 18; Conservative 7; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 VGIDLETVKOVKETIAIFAGTEKVEALLAISNMHKN 323
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LOCATION: (1)..(103)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT; ORGANISM: Clostridium difficile US-10-282-122A-52947
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Indels

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RESULT 11 US-10-059-720-11 Sequence 11, Application US/10059720 ; Fublication No. US20030027314A1

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Gaps

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US-09-934-868-8

Sequence 8, Application US/09934868

Patent No. US2002013190A1

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: APPLICANT: Admes M

APPLICANT: Schenzle, Andreas J

TITLE OF INVENTION: DEMITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CLIS 60 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

PRIOR FILING DATE: 2001-08-22

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SEQ ID NO S

LENGTH: 618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 28.4%; Score 55; DB 9; Length 618; Best Local Similarity 34.5%; Pred. No. 1.6e+02; Matches 10; Conservative 8; Mismatches 11; Indels
  34.5%; Pred. No. 1.6e+02;
tive 8; Mismatches 11; Indels
                                                                        11 ETLOKOKETIKAFLKKLEALMASNDNANK 39
                                                                                                      23 QVIARSRETRAAYLKRIEAAIAEGPQRNK 51
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ne : 47.3142 secs
    Best Local Similarity 34.5
Matches 10; Conservative
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; ORGANISM: METHYLOMONAS SP.
US-09-934-868-8
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CTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (236)
COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-891-2917
                                                                                                                                                                      Gaps
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APPLICANT: Koffas, Mattheos
APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Odom, J. Martin
APPLICANT: Ve, Rick
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REPERENCE: CL1619 US NA
CURRENT APPLICATION NUMBER: US/09/934,901
CURRENT APLICATION NUMBER: US/09/29,906
PRIOR FILING DATE: 2001-08-22
PRIOR FILING DATE: September 1, 2000
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 618
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PCOO.
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ 1D NOS: 10231
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 28.4%; Score 55; DB 10; Length 240; Best Local Similarity 36.4%; Pred. No. 54; Matches 12; Conservative 7; Mismatches 14; Indels
                                                                                                                    28.4%; Score 55; DB 17; Length 217; 46.2%; Pred. No. 48;
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                      ; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_8374C.1.pep
US-10-425-115-351517
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                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                            9 DAETLÓKÓKETIKAFLKKLEALMASN 34
                                                                                                                                                                                                                                                                                                                                                                        Sequence 2917, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
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Sequence 18, Application US/09934901
Fatent No. US20020110885A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                        Best Local Similarity
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                         US-09-764-891-2917
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LENGTH: 240
                                                                                                                    Query Match
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

November 10, 2004, 13:40:53 ; Search time 9.81132 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-52 194 1 ASWAPVGRDAETLQKQKETIKAFLKKLEALMASNDNANKT 40 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Searched:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* 1 2 E 4 Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

·		æ (SUMMAKIES	
	Score	Query Match	Length	DB		Description
	5.00	30.4	833	. 2	148283	gene CC2 protein -
	57.5	29.6	554	7	C82743	rans
		σ	247	8	F84004	hypothetical prote
	57	g	318	~	G82416	
	57	29.4	419	7	A25438	keratin, type I cy
	9	29.1	447	~	F75164	dnag-lik
	56.5	29.1	447	7	E71177	tical
	26	28.9	29	7	C90519	hypothetical prote
	56	8		Н	S02041	=
	52	28.4		7	A56694	keratin, type II,
	22	ø		~	T25068	Ω Π,
	55	28.4		N	I54383	chromosome segreda
	52	28.4		N	T30534	chromosome segrega
	55	28.4		~	T23433	
	ស	28.4		7	T37316	probable laminin a
	ស	œ		7	T42993	probable spectrin
	22	28.4	4101	7	T23630	٠н
	54.5	æ		7	T13734	
	54	27.8		~	T21815	hypothetical prote
	54	Γ		7	G83254	м
	54	~		N	D81322	ர
	54	~		-1	A27605	3
	23	7		N	56	outer surface prot
	53	7		7	4028	face
	53	7		~	vo	ribosomal protein
	53	27.3		~	F69378	conserved hypothet
	23	~		7	64	hypothetical prote
	23	7		~	Φ	Ξ.
	23	27.3	1188	N	T19552	he

dystrophin - mouse	hypothetical prote	keratin-like prote	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	chromosome-associa	D1 protein homolog	hypothetical prote	hypothetical prote	hypothetical prote	hypothetical prote	translation releas	conserved hypothet	hypothetical prote
828916	855150	I38025	T13010	D72317	T04501	T26695	T23744	T02636	T26963	T26964	T23040	E97138	E64403	A82132	T19460
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3678	173	257	274	377	398	915	1244	1274	3450	3461	232	279	425	233	286
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27	27.	26.	26.	26.	26.	26.	26.	26.	26.8	26.	26.	26.	26.	26.	26
53	52.5	25	52	52	52	52	52	52	25	52	51.5	51.5	51.5	51	51
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Jackson CC2 protein - mouse (fragment)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Species: Mus musculus (house mouse)
C,Accession: 148283
R,Maucuer, A.; Camonis, J.H.; Sobel, A.
R,Maucuer, A.; Camonis, J.H.; Sobel, A.
A,Accession: 148283
A,Accession: 148283
A,Accession: 148283
A,Accession: 148283
A,Status: preliminary; translated from GB/EMBL/DbJJ
A,Molecule type: mRNA
A,Residues: 1-83 <RES>
A,Cross-references: EMBL:X82319; NID:G791075; PIDN:CAA57762.1; PID:G791076
C,Genetics: A,Gene: CC2
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RESULT 2

ABC transporter ATP-binding protein XF0944 [imported] - Xylella fastidiosa (strain 9a5c C; Species: Xylella fastidiosa
C; Species: Xylella fastidiosa
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C; Species: The Xylella fastidiosa
C; Species: The Xylella fastidiosa
C; Species: Mullo: 20365717; PMID: 10910347
A; Note: for a complete list of authors see reference number A59328 below
A; Accession: C82743
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4 APVGRDAETLQKQKETIKAFLKKLEALMASNDN 36
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A; Residues: 1-447 < KAW>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein BH2838 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Accession: F84004
R;Accession: F84004
R;Takami, H; Nakasone, K; Takaki, Y; Maeno, G; Sasaki, R; Masui, N; Fuji, F; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Itles: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: F84004
A;Accession: F84004
A;Accession: F84004
A;Accession: F84004
A;Accession: F84004
A;Accession: L247 < STO>
A;Residues: 1-247 < STO>
A;Residues: 1-247 < STO>
A;Cross-references: UNIPROT:09K913; GB:AP001516; GB:BA000004; NID:gl0175192; PIDN:BAB065
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH2838
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Affile: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82035; MUD:20406833; PMID:10952301

A; Reference number: A82035; MUD:20406833; PMID:10952301

A; Residues: Draiminary
A; Molecule type: DNA
A; Residues: Using CHEI
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A; Residues: Using CHEI
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A; Residues: Using CHEI
A; Resperimental source: serogroup 01; strain N16961; biotype El Tor
P.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A.A.tuthors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z., Contents: annotation G., Genetics: annotation G., Superismily: Arp-binding cassette homology
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Pred. No. 18;
7; Mismatches 13; Indels
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Pred. No. 14;
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29.6%; Score 57.5; I
Best Local Similarity 40.0%; Pred. No. 28;
Matches 14; Conservative 7; Mismatches
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Best Local Similarity 38.7%
Matches 12; Conservative
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Best Local Similarity 39.4
Matches 13; Conservative
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hypothetical protein PH1699 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Accession: E71177
R;Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
M; Ohfuku, Y; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguch
DNA, Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
A;Title: Complete Sequence and gene organization of the genome of a hyper-thermophilic
A;Accession: E71177
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
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submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome str
A;Reference number: A75001
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A.Experimental source: strain Orsay
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A,Residues: 1-419 <MIX>
A,Fross-references: UNIPROT.P05781, GB:M18155, GB:X05865, NID:g214558, PID:g214560
C,Superfamily: cytoskeletal keratin
C,Keywords: coiled coil
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H
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C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
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J. Cell Biol. 103, 1957-1965, 1986
Afritle: Stage-specific keratins in Xenopus laevis embryos and
A;Reference number: A25438; MUID:87057649; PMID:2430981
A;Accession: A25438
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OB
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29.4%; Score 57; DB
Best Local Similarity 35.7%; Pred. No. 24;
Matches 10; Conservative 9; Mismatches
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Best Local Similarity 44.4%;
Matches 16; Conservative
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A;Title: A 230kb cosmid walk in the Duchenne muscular dystrophy gene: detection of a co A;Reference number: S09071; MUID:88067745; PMID:2825128
A;Accession: S71487
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 222-281 cHEI>
C;Comment: Dystrophin is proposed to play a role in anchoring the cytoskeleton to the p C;Comment: Defects in dystrophin are responsible for the Duchenne/Becker muscular dystro;Superfamily: dystrophin, alpha-actinin actin-binding domain homology; spectrin/dystro;Keywords: actin binding; calmodulin binding; cytoskeleton; leucine zipper; membrane-a F;18-237/Domain: alpha-actinin actin-binding domain homology cACT>
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C.Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C.Bate: 21-Uul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
C.Accession: A56694
R.Powell, B.C.; Crocker, L.A.; Rogers, G.E.
DNA Seq. 3, 401-405, 1993
A.Title: Complete sequence of a hair-like intermediate filament type II keratin gene.
A.Title: Complete sequence of a hair-like intermediate filament type II keratin gene.
A.Title: Complete Sequence of a hair-like intermediate filament type II keratin gene.
A.Title: Day A.Accession: A56694
A.Status: preliminary
A.Molecule type: DNA
A.Residues: 1-480 <br/>A.Residues: 1-480 <br/>A.Schous Pows
A.Complete Complete                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig3-337/Region: hinge
Fig8-337/Region: hinge
Fig8-337/Region: hinge
Fig80-49/Domain: spectrin/dystrophin repeat homology <8P01>
Fig80-489/Domain: spectrin/dystrophin repeat homology <8P03>
Fig80-689/Domain: spectrin/dystrophin repeat homology <8P03>
Fig80-689/Domain: spectrin/dystrophin repeat homology <8P03>
Fig80-689/Domain: spectrin/dystrophin repeat homology <8P04>
Fig80-986/Domain: spectrin/dystrophin repeat homology <8P05>
Fig80-986/Domain: spectrin/dystrophin repeat homology <8P05>
Fig80-986/Domain: spectrin/dystrophin repeat homology <8P05>
Fig80-1366/Domain: spectrin/dystrophin repeat homology <8P05>
Fig80-1369/Domain: spectrin/dystrophin repeat homology <8P05>
Fig80-1266/Domain: spectrin/dystrophin repeat homology <8P10>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P10>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P12>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P15>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P25>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P22>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P22>
Fig80-1270/Domain: spectrin/dystrophin repeat homology <8P23>
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A;Introns: 140/3; 210/2; 230/3; 262/3; 317/3; 359/3; 433/2; 444/1
C;Superfamily: cytoskeletal keratin
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Pred. No. 3.1e+02;
7; Mismatches 8; Indels
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F;3052-3089/Domain: WW repeat homology <WW1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;3481-3502/Region: leucine zipper motif
F;3547-3568/Region: leucine zipper motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              keratin, type II, KRT2.13 - sheep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28.9%;
1 Similarity 40.0%;
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28.48;
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Best Local
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dystrophin, muscle - chicken

NyAlternate names: duchenne muscular dystrophy protein

C;Species: Gallus gallus (chicken)

C;Date: 07-Sep-1990 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Date: 07-Sep-1990 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Date: 07-Sep-1990 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004

C;Accession: S02041; S02013; S71487

R;Lemaire, C; Heilig, R.; Mandel, J.L.

A;Arterence number: S02041; MUD: 89098331; PMID: 3062582

A;Arcession: S02041

A;Reference number: S02041; MUD: 89098331; PMID: 3062582

A;Reference number: S02041

A;Residues: 1-3660 *LEM

A;Residues: 1-3660 *LEM

A;Residues: 1-3660 *LEM

A;Reference number: S02013; MUD: 89210800; PMID: 3072195

A;Reference number: S02013; Mudel, J.L.

B;Heillg, R.; Lemaire, C.; Mandel, J.L.

R;Heillg, R.; Lemaire, C.; Mandel, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nyothetical protein MYPU_0590 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90519
C;Date: 24-May-2001 #text_change 09-Jul-2004
C;Accession: C90519
C;Accession: C90519
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: C90519
A;Accession: C90519
A;Accession: C90519
A;Accession: C90519
A;Accession: C90519
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A;Accession: C90519
A;Accession: C90519
C;Genetics: C90519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 447;
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Pred. No. 22;
5; Mismatches 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 56.5; DB
Pred. No. 29;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 42.9%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 29.1%;
Best Local Similarity 44.4%;
Matches 16; Conservative
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A;Genetic code: SGC3
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Ririboldi Tunnicliffe, G.R.; Platzer, M.; Nyakatura, G.; Elgar, G.S.; Brenner, S.; Rosei submitted to the EMBL Data Library, September 1997
A;Description: Analysis of the genomic loci of Fugu rubripes homologs of the human dises A;Reference number: 220848
A;Reference number: 220848
A;Reference number: 220848
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1233 < AIIB>
A;Residues: 1-1233 < AIIB>
A;Cross-references: UNIPROT: 073696; EMBL: AF026198; NID: g3098263; PID: g3098266; PIDN: AAC: C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A, Residues: 1-3672 <WIL>.
A, Cross-references: UNIPROT:Q21313; EMBL:Z70286; PIDN:CAA94293.1; GSPDB:GN00022; CESP:K
A, Experimental source: clone K08C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Map position: IV
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3;
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Map position: 4
A;Introns: 66/1; 284/3; 563/1; 1187/3; 1248/3; 1300/1; 1460/1; 1623/3; 2361/3; 2988/3;
C;Superfamily: laminin alpha-1 chain; laminin G repeat homology; laminin-type EGF-like
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T37316
R;Joh, K; Zhu, K; Hedgecock, B.M.; Inoue, T.; Hori, K.
submitted to the EMBL Data Library, August 1998
A;Description: Laminin alpha chain gene in the nematode C. elegans.
A;Reference number: 221681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein KOBC7.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-3704 <JOH>
A;Cross-references: UNIPROT:P91904; EMBL:AB016806; PIDN:BAA32347.1
A;Experimental source: strain N2
                                                                                                                                                                                                                                                                                                                                           28.4%; Score 55; DB 2; Length 1233; ilarity 42.1%; Pred. No. 1.3e+02; Conservative 5; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3672;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :|:| ||: : ||| || 324
287 KDSELNOKRPQYIKAKENTSHKIKKLEAARKSLQNAQK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8 RDAETLOKOKETIKA-----FLKKLEALMASNDNANK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probable laminin alpha chain - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 55; DB 2; I
Pred. No. 4.2e+02;
7; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6 VGRDAETLOKOKETIKAFLKKLEALMASNDNANK 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted to the EMBL Data Library, March 1996
A; Reference number: 219740
A; Accession: T23433
A; Status: preliminary; translated from GB/EMBL/DDBJ
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A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28.4%;
ilarity 38.2%;
Conservative
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A, Gene: CESP: K08C7.3
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C; Accession: T30534
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                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, May 1996

A;Reference number: Z19977

A;Accession: T25068

A;Status: pression: T25068

A;Status: pression: T25068

A;Geoule type: DNA

A;Residues: 1-1065 <WIL>
A;Cross-references: UNIPROT:Q22639; EMBL:Z73098; PIDN:CAA97331.1; GSPDB:GN00023; CESP:T2

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. Accession: 154383
R.Rocques, P.J.; Clark, J.; Ball, S.; Crew, J.; Gill, S.; Christodoulou, Z.; Borts, R.H. Hum. Mol. Genet. 4, 243-249, 1995
A.Title: The human SB1.8 gene (DXS423E) encodes a putative chromosome segregation proteil A.Reference number: 154383
A.Accession: 154383
A.Accession: 154383
A.Accession: 154383
A.Accession: 154383
A.Accession: 154383
A.Accession: 154383
A.Resiones: 1-1233
A.Resiones: 1-1233
A.Resiones: 1-1233
A.Resiones: GB:S78271; NID:g999379; PIDN:AAB34405.1; PID:g999380
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                                                                                                                                                                                                                                                                C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25068
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C,Species: Fugu rubripes (Japanese pufferfish)
C,Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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A;Map position: 5
A;Introns: 67/2; 147/2; 207/3; 242/3; 293/3; 825/2; 897/1; 1032/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 28.4%; Score 55; DB 2; Length 1065; Best Local Similarity 40.0%; Pred. No. 1.1e+02; Matches 10; Conservative 8; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1233;
                            Indels
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                            15;
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. 1.3e+02;
                                                                                                                          323 ATVNRHGETLRRTKEEINELNRLIQRLTAEIENA 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Genetics:
A;Gene: GDB:XIAA0178; SMC1; SB1.8/DXS423E
A;Cross-references: GDB:9785049
A;Map position: Xpter-Yqter
C;Superfamily: chromosome segregation protein SMC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Mismatches
                                                                                       4 APVGRDAETLQKQKETIKAFLKKLEALMASNDNA
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Pred. No.
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Best Local Similarity 42.1%;
Matches 16; Conservative
38.2%;
                            Conservative
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                            13;
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T30534
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Gaps

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Query Match 28.4%; Score 55; DB 2; Length 3704;
Best Local Similarity 38.2%; Pred. No. 4.2e+02;
Matches 13; Conservative 7; Mismatches 14; Indels 0; Gaps
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Search completed: November 10, 2004, 14:52:21 Job time : 10.8113 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

November 10, 2004, 13:38:57; Search time 53.283 Seconds (without alignments) 431.938 Million cell updates/sec Run on:

US-10-092-750-52 194 1 ASMAPVGRDAETLQKQKETIKAFLKKLEALMASNDNANKT 40 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1825181 seqs, 575374646 residues Searched:

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	hou	mus mu		91zue mus			o hor	homo sa	homo	Q6n8h1 rhodopseudo	Cae27373 rhodopseu	Q9lvq4 arabidopsis	Q8jip4 coturnix co	Q8chg3 mus musculu		Q73al3 bacillus ce	Aas40688 bacillus	Q8stn2 encephalito	Q8rn37 campylobact	Q6hkrl bacillus th	Q61be4 mus musculu	Caa57762 mus muscu		Q8ri43 fusobacteri	xenopus l	drosophil	drosophil	gratiol	Q8sm17 pennelliant	xylella fa	Q9pet4 xylella fas
	BPEA_HUMAN	062059	BAC98011	BPA1 MOUSE	MACF_MOUSE	Q89Q <u>T</u> 6	BAA32310	MACF_HUMAN	MAC4 HUMAN	Q6N8 <u>H</u> 1	CAE27373	Q9LVQ4	Q8J1P4	GCC2_MOUSE	Q82X <u>2</u> 3	Q73AL3	AAS40688	QBSTN2	QBRN37	Q6HKR1	Q6LBE4	CAA57762	Q7P7A7	QBRI43	Q7ZTJ9	DMDB DROME	DMDA_DROME	Q7 <u>YKQ</u> 3	Q8SM17	7.A	Q9PET4
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## ALIGNMENTS

RESULT 1

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4	OBNBJ3: OBWXK9: 096A
) E	2001 (Rel, 40, Created)
Б	28-FEB-2003 (Rel. 41, Last sequence update)
Д	01-OCT-2004 (Rel. 45, Last annotation update)
DE	(Trabeculin
ЭE	(Bullous pemphigoid antigen) (BPA) (Hemidesmosomal plaque protein)
E :	
S :	PAG1, DMH,
s o	
0	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleoscomi;
8	Primates;
š	NCBI_TAXID=9606;
N S	
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χ:	TISSUE=KETAUTHOCYTEB;
X :	MEDLINE=Z1839LII; PUDMEQ=II/S1855; DOI=10:10/4/ JDC:MI09Z09Z00;
\$ 1	Oxumura M., Yamakawa H., Onara U., Owaribe K.;
Y E	brace (bullous pemphilyota amerycan)
7 F	sery retaced to the
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ן אַ	11550b=Duoquium;
XX:	MEDLINE=2238825/; Pubmed=124//932; DOI=10:10/3/pida:242003039;
RA I	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Snenmen C.M., Schuler G
RA:	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhar N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang U., Halen F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Kubin G.M., Hong L.,
KA	Casavant 1.L., scheetz
KA	., Carninci P., Prange
K.	Abramson k.D., Mullany
KA	Malek J.A., Gunarathe F.
Z.	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.U., Hulyk S.W.,
Z.	
KA	Fahey J., Helton E., Ketteman M., Madan A., Kodrigues S., Sanchez A.,
RA F	Whiting M., Madan A., Young A.C., Shevenenko
<b>S</b> :	Blakesley K.W., Touchman J.W., Green E.D., Dickson M.C.,
RA :	Rodriguez A.C., Grimmood J., Schmucz J., Myers K.M.,
KA :	SKalska U., Smallus
KA	., Marra M.A.;
R.	"Generation and initial analysis of more than 15,000 rull-length numan
RT	and mouse cDNA sequences.";
Z.	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Z :	[3]
저 t 가 (	SEMODENCE OF 1.702-4155 FROM N. (150FORM 9).
3 k	TISSUBERFRIIN, FISCENCE, AND TORIQUE; Pubbooks Indiano Indiano (1000 / 100 )
ž :	Crumedatt/Occasional Trie D
\$ ;	OCA T., SUZUKI T., NISHIKAWA I., OCAUKI T., SUSUKI T., SUZUKI T., TITE A.,
R.A	א איים אייר manatsu A., Hayasnı K., Sato H., Nagaı K., א איי המאברם א., א Mayasnı K.,

IsoId=Q03001-2; Sequence=External;

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RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S., RA Yamanoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y., RA Agadhari K., Murakani K., Yasuda T., Iwayanagi T., Wagateuma M., Shiratori A., Sudo H., Kanda K., Kaku Y., Kodaira H., Kondo H., RA Omura Y., Abe K., Kamihara K., Kateuta N., Sato K., Tanikawa B., RA Omura Y., Abe K., Ishibashi T., Yamashita H., Murakawa K., Raihara K., Ishibashi T., Yamashita H., Murakawa K., Raihara K., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Rana M., RA Ishida S., Ono Y., Takiguchi S., Watanabe M., Hiraoka S., Chiba Y., Rana M., RA Momura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., RA Imose N., Musashino K., Yuuki H., Oshima A., Sasaki N., Abtrika S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O., RA Marayawa S., Senoh A., Mizoguchi H., Goto Y., Shiobata N., Saro S., Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H., RA Habilgaki H., Watanabe K., Kumagai A., Takemoto M., Pukuzumi Y., Rawabata R., Hikiji T., Kobatake N., Hirao M., Ohmori Y., Rawabata A., Hikiji T., Kobatake N., Hirao M., Ohmori Y., Rawabata A., Hikiji T., Kobatake N., Hirao M., Ohmori Y., Rawabata A., Hikiji T., Kobatake N., Hirao M., Ohmori Y., Rawabata A., Hikiji T., Kobatake N., Hirao M., Ohmori Y., Rawabata A., Hata H., Watanabe M., Komatsu T., Nagashi T., Oyama M., Hata H., Watanabe M., Komatsu T., Nakagawa S., Rah Rawabata R., Nakajima Y., Matanabe M., Komatsu T., Nawasimu K., Nakajima Y., Matanabe M., Komatsu T., Nawai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S., R., Complete sequencing and characterization of 21,243 full-length human C., Naka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Keratinocytes;

MEDLINE=92011493; PubMed=1717441;

MEDLINE=92011493; PubMed=1717441;

MEDLINE=92011493; PubMed=1717441;

Sawamura D., Li K., Chu M.-L., Uitto J.;

"Human bullous pemphigoid antigen (BPAG1). Amino acid sequences
deduced from cloned cDNAs predict biologically important peptide
segments and protein domains."

J. Biol. Chem. 266:17784-17790(1991).

-:- FUNCTION: Cytoskeletal linker protein. Anchors keratin-containing
intermediate filaments to the inner plaque of hemidesmosomes. The
proteins may self-aggregate to form filaments or a two-dimensional
mesh (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T., "Construction of expression-ready cDNA clones for KIAA genes: manual curation of 330 KIAA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDLINE=99087487; PubMed=9872452;
Magase T., Ishikawa K.-I., Suyama M., Kikuno R., Miyajima N.,
Nagase T., Ishikawa K.-I., Suyama M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes. XI.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro.";
[6]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBUNIT: Homodimer (By similarity).
-!- SUBCELLUTAR LOCATION: Cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Event=Alternative splicing; Named isoforms=10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 3535-5171 FROM N.A. (ISOFORM 6).
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IsoId=094833-2; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1;
IsoId=Q03001-1; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=22158633; PubMed=12168954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nat. Genet. 36:40-45(2004).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 113810; ...
MIM; 600088; ...
GO; GO:0005737; C:cytoplasm; ISS.
GO; GO:0005200; F:structural constituent of cytoskeleton; ISS.
GO; GO:0045104; P:intermediate filament cytoskeleton organiza. . .; ISS.
                                                                                                                                                                                                           ISOId=094833-1; Sequence=VSP_005066, VSP_005067;
Note=NO experimental confirmation available;
Note=NO experimental confirmation available;
-!-ISSUE SPECTFICTY: Highly expressed in skeletal muscle and cultured keratinocytes.
-!-BASAE: BARAI: Ba nautoantigen of bullous pemphigoid
-!-SIMILARITY: Belongs to the plakin or cytolinker family.
-!-SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!-SIMILARITY: Contains 29 spectrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R InterPro; IPRO10948; EF-Hand_like.
R InterPro; IPRO10948; EF-Hand_like.
R InterPro; IPRO10948; EF-Hand_like.
R InterPro; IPRO10152; SH3.
R InterPro; IPRO02107; Spectrin.
R Pfam; PF00036; efhand; 2.
R Pfam; PF00187; Spectrin.
R Pfam; PF00187; Spectrin.
R Pfam; PF00187; Spectrin.
R Pfam; PF00187; Spectrin.
R SMART; SM00054; EFh; 2.
R SMART; SM00150; EF-Hand; 1.
R SMART; SM00150; SFEC; 30.
R R SMART; SM00150; SFEC; 30.
R Actin-binding, Alternative splicing; Antigen; Calcium;
M Actin-binding, Cell adhesion; Colled coil; Cytoskeleton; Repeat;
W SH3 domain; Structural protein.
                                                                                                                                                                              IsoId=094833-3; Sequence=VSP_005068, VSP_005069;
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Spectrin 2.
Spectrin 3.
SH3.
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Spectrin 6.
Spectrin 7.
Spectrin 7.
              Name=3; Synonyms=1e;
IsoId=Q03001-3; Sequence=External;
                                                            IsoId=Q03001-4; Sequence=External;
                                                                                                      Name=7; Synonyms=EB;
IsoId=Q8WXK8-2; Sequence=External;
                                                                                                                                                  IsoId=Q03001-6; Sequence=External;
                                                                                       IsoId=Q03001-5; Sequence=External;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL, AF400226, AAL62061.1;
EMBL, BC016911, AAH16991.1;
EMBL, AKC55169, BAB70870.1;
EMBL, AKC94683; BAC04449.1;
EMBL, AKC94683; BAC04449.1;
EMBL, AKC96713; BAC04449.1;
EMBL, AL137089; CAC12899.1;
HSSP, O82040; 1K9U.
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Query Match
Best Local Similarity
Matches 30; Conserv
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Saga Y., Nagase T., Ohara O., Koga H.;

"Prediction of the coding sequences of mouse klaA-homologus of mouse complete mucleotide sequences of 500 mouse KIAA-homologus of DNAs identified by screening of terminal sequences of cDNA clones randomly sampled from size-fractionated libraries.";

DNA Res. 10:167-180(2003).

EMBL; AK122201; BAC98011.1; -.

GO; GO:0030056; C:hemidesmosome; IDA.

GO; GO:0030056; C:hemidesmosome; IDA.

GO; GO:0030050; P:retrograde axon cargo transport; IMP.

Ffam; PF00415; Spectrin.

Ffam; PF00415; Spectrin.
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TISSUE=Embryonic tail;
TASAZAKI N., Kikuno R., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
Saga Y., Nagase T., Ohara O., Koga H.;
"Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI _TaxID=10090;
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Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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llarity 78.9%; Pred. No. 1.8e-09;
Conservative 5; Mismatches 3; Indels
                                                                                        Score 190; DB 1; Length 5171;
                                                                                                  No. 1e-13;
No. 1e-13;
O; Indels
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Spectrin 9.
Spectrin 10.
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SEQUENCE OF 6699-7389 FROM N.A. (ISOFORNS 3 AND 4).

SEQUENCE OF 6699-7389 FROM N.A. (ISOFORNS 3 AND 4).

STRAIN-C57BL/6J; TISSUE-Fetal skin, and Fetal spinal cord;

MISLINE-257B4683; PubMed=1246681; DOI=10.1038/nature012665.

RA ASIA, Furuno M., Kaaukawa T., Adachi J., Bono H., Kondo S.,

RA AND KARADI I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Baldarelli R., Hill D.P. Bult C., Hume D.A., Ouackenbush J.,

Baldarelli R., Hill D.P., Bult C., Hume D.A., Ouackenbush J.,

Baldarelli R., Fletcher C., Hume D.A., Consins S.,

RA Bala E., Dragani T.A., Fletcher C.F., Corbain L.E., Cousins S.,

RA Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,

RA Anai A., Kawaji H., Kawasawa Y., Kadzierski R.M., King B.L.,

RA Anai A., Kawaji H., Kawasawa V., Kadzierski R.M., King B.L.,

RA Magashma T., Numata K., Marchionni L., McKenzie L., Miki H.,

RA Nagashma T., Numata K., Pontius J.U., Oi D., Ramachandran S.,

RA Nagashma T., Numata Y., Taylor M.S., Teasdale R.D., Tomita M.,

RA Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,

Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,

Namani L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang I.,

Yana Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

Hircane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Hircane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hircane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,

RA Hara A., Hashizume W., Materston R., Lander E.S., Rogers J.,

RA Hara A., Hashizaki Y.,

RA Hara A., Hashizame W., Sato K.,

Barnishi A., Soshino M., Waterston R., Lander S.S., Rogers J.,

RA Harayasis C the mouse transcriptome based on functional annotation of R. Go, 770 full-length convas.",

RA Harukayasis G the mouse transcriptome based on functional annotation of R. Constant M. A. (2002).
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091276; 0912U7;
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
01-0CT-2004 (Rel. 45, Last annotation update)
Bullous pemphigoid antigen 1, isoforms 1/2/3/4 (BPA) (Hemidesmosomal plaque protein) (Dystonia musculorum protein) (Dystonia musculus (Mouse).
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STRAIN=BALB/c; TISSUE=Muscle, and Neuron;
MEDLINE=21465767; PubMed=11514586; DOI=10.1083/jcb.200012098;
Leung C.L., Zheng M., Prater S.M., Liem R.K.H.;
"The BPAG1 locus alternative splicing produces multiple isoforms with distinct cytoskeletal linker domains, including predominant isoforms
III. The Complete Nucleotide Sequences of 500 Mouse KIAA-homologous cDNAs Identified by Screening of Terminal Sequences of CDNA Clones Randomly Sampled from Size-fractionated Libraries."; DNA Res. 10:167-180(2003).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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SMART; SMO0150; SPEC; 32.
PROSITE; PRO0019; ACTININ 1; 1.
PROSITE; PSO0019; CT: CH; 2.
PROSITE; PSO0018; EF HAND; 2.
Actin-binding; Alternative splicing; Calcium, Calcium-binding; Cell adhesion; Colled coil; Cytoskeleton; Repeat; SH3 domain; Structural protein.
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   EMBL; AF936879; AAK83384.1; ...

REMEL; AF936879; AAK83383.1; ...

REMEL; AK051626; BAC34695.1; ...

REMEL; AK051626; BAC34695.1; ...

REMEL; AK051626; BAC34695.1; ...

REMEL; AK05167; Cortoplasm; ISS.

RGO; GO:0005200; F:structural constituent of cytoskeleton; ISS.

GO; GO:0005200; F:structural constituent of cytoskeleton organiza...; ISS.

RO; GO:0005200; F:structural constituent of cytoskeleton organiza...; ISS.

RGO; GO:0005200; F:structural constituent of cytoskeleton; ISS.

RGO; GO:0005200; F:structural constituent of cy
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                                                                                                                                                                                                                                                                                                                                 -!- FUNCTION: Cytoskeletal linker protein. Anchors keratin-containing intermediate filaments to the inner plaque of hemidesmosomes. The proteins may self-aggregate to form filaments or a two-dimensional mesh (By similarity).
-!- SUBUNIT: Homodimer. Interacts with the neuronal intermediate filament protein, Proh (By similarity).
-!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
-!- ALTERNATIVE PRODUCTS:
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Note=No experimental confirmation available;
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Note=No experimental confirmation available;
                                                                                                                                             Name=2; Synonyms=b;
IsoId=Q91ZU6-1; Sequence=Displayed;
Name=1; Synonyms=a;
IsoId=Q91ZU6-2; Sequence=VSP_050483;
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IsoId=Q91ZU8-1; Sequence=External;
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(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).

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EMBL; U67205; AAC52990.1;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to licenseeleb-sib.ch).
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STRAIN=BALB/c;
MEDLINE=20069791; PubMed=10601340;
Leung C.L., Sun D., Zheng M., Knowles D.R., Liem R.K.H.;
"Microtubule actin cross-linking factor (WACF): a hybrid of dystonin and dystrophin that can interact with the actin and microtubule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         isoid=Q9QXZ0-3; Sequence=VSP 000718;
-!- TISSUE SPECIFICITY: Expressed mainly in lung, brain, spinal cord,
                                                                                                                                                                                                                                                                                                    MACF_MOUSE STANDARD; PRT; 5327 AA.
Q9QXZ0; P97394; P97395; P97396;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
Microtubule-actin crosslinking factor 1 (Actin cross-linking family
                                                                                                                                                                                                                                                                                                                                                                                                                                                             7)
Mame-Macfi; Synonyms-Macf, Acf7, Aclp7;
Mus musculus (Mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                         ..
                     Length 7389;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          skeletal and cardiac muscle, and skin.
-!- SIMILARITY: Contains 1 actin-binding domain.
-!- SIMILARITY: Contains 2 calponin-homology (CH) domains.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!- SIMILARITY: Contains 1 SH3 domain.
-!- SIMILARITY: Contains 37 spectrin repeats.
                                                                       3; Indels
                                                                                                                                                         5123 MAPVGRDAETLRKQKACMQTFLKKLEALMASNDSANRT 5160
                                                                                                                           3 MAPVGRDAETLOKOKETIKAFLKKLEALMASNDNANKT 40
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                   ch 77.8%; Score 151; DB 1;
1 Similarity 78.9%; Pred. No. 8.7e-09;
30; Conservative 5; Mismatches 3;
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Note=Incomplete sequence;
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IsoId=Q9QXZ0-1; Sequence=Displayed;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                microtubules.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS:
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J. Cell Biol. 147:1275-1286(1999).
[2]
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EMBL; U67203; AAC52988.1; -.
EMBL; U67204; AAC52989.1; -.
                   Query Match
Best Local Similarity
Matches 30; Conserv
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Hisspi, Q15149; 1MBB.

MGD; MG1:108559; Macfil.

MGD; MG1:108559; Macfil.

MGD; MG1:108559; Macfil.

MGD; MG1:108559; Macfil.

GO; GO:0015629; C:actin cytoskeleton; IDA.

GO; GO:0008017; F:actin binding; IDA.

GO; GO:0008017; F:microtubule cytoskeleton; IDA.

GO; GO:0008017; F:microtubule binding; IDA.

GO; GO:0008017; F:microtubule binding; IDA.

GO; GO:0001189; F:microtubule binding; IDA.

RICEPPO; IPRO01189; EF-hand.

RICEPPO; IPRO01093; EF-Hand_like.

RICEPPO; IPRO01452; SH3.

RICEPPOSITE; SH3.

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TISSUE=Brain;
MEDLINE=98116662; PubMed=9455484;
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DNA Res. 4:345-349(1997).

EMBL, AB007934; BAA32310.3; -..

SEQÜENCE 4433 AA, 505640 MW:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIAA0465 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
Pfam; PF00512; HisKA; 1
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Nomura N., Ohara O.;
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AC 990PN3; 0750

DT 16-0CT-2001

DT 16-0CT-2001

DT 05-UL-2004

DE MICTORUNION

DE ACALIN-bindin

GN Name=MACF1;

CS HOMO SADIENS

CO NCBI_TAXID=9

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RN SEQUENCE FRC
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Eradyzhizobium japonicum USDA110.";

Eradyzhizobium japonicum USDA110.";

IL DNA Res. 9.189-197(2002).

-!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).

-!- SIMILARITY: Contains 1 histidine kinase domain.

R ROJ GO:0016021; C:integral to membrane; IEA.

R GOJ GO:0016224; F:ATP binding; IEA.

R GOJ GO:0016301; F:kinase activity; IEA.

R GOJ GO:0016301; F:kinase activity; IEA.

R GOJ GO:0016301; F:kinase activity; IEA.

R GOJ GO:0016301; F:two-component sensor molecule activity; IEA.

R GOJ GO:000165; P:sensory perception; IEA.
                                                                                                                   TLEWALLECKTRKSQDSVLDPAERAVYRVADERBRYVÇKK
TPTKRYNKHLMKVRKHINDYEDLRDCHNISLLEVLSGIK
TPTKRYNKHLMKVRKHINDYEDLRDCHNISLLEVLSGIK
NERKGRMRPHRLQNVQIALDFLKQRQVKLNNIRNDITDG
NPKLTLGLIWTILIHFQ -> MGNSLGCVKBPKBSIAVPEK
APISPKKRVRFKRKRRGKKILTPEASHREEALBGTGVIEET
                                                                                                                                                                                                                                         ETTIKLTARLEKEBGYGGAEHPPSDIFLEGDSAPNSGYGDQ
GMIVOYKESTQAEIQTAHLLLENESSYVGGAMDSLEEGMTV
TAHLLDNPAERNCKESVOLVEFPRTASCSSRAVLLPLQGE
TAVEGGGTLLRHRHSSTLRRTDYPSETYDQDQPSEGWSVG
GRTKSVPSAPPTGSWIAKCSVASSIPKQSGDFIHTEPTHVG
  MSSSDEETLSERSCRSERSCRSERSYRSERSGSLSPCPPGD
TLPWNLPLHEQKKRKSQDSVLDPAERAVVRVA -> EKEFV
                                                                            /FTId=VSP_000717.
MSSSDEETLSERSCRSERSCRSERSYRSERSGSLSPCPPGD
                                                                                                                                                                                                                                                                                                                                                                    LVSCKGPIMPASQSDLSVSGITVSILPSSSGYGSDGLRLHG
IRPEDTEPEKTSTPFSEEDGTLSLE (in isoform 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=22484998; PubMed=12597275;
Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
Tabata S.;
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Pred. No. 23;
7; Mismatches 8; Indels
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Bradyrhizobiaceae, Bradyrhizobium
                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=VSP 000718.
L -> P (in Ref. 2; AAC52990).
Q -> H (in Ref. 2).
MW; SDB4FFSA6514BFFA CRC64;
                                                   QAYEDVLERYK (in isoform 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-070-2003 (TrEMBLrel. 24, Created)
01-070-2003 (TrEMBLrel. 24, Last sequence update)
01-070-2004 (TrEMBLrel. 26, Last annotation update)
Two-component sensor histidine kinase.
OrderedLocusNames=blr3132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           486 AA
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Interpro; IPR003661; His kinA N.
Interpro; IPR09085; His kin homodim.
Pfam; PF00672; HAMP; 1.
Pfam; PF02518; HATPase_c; 1.
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InterPro; IPR004358; Bact sens pr_C.
InterPro; IPR003660; HAMP.
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1882 1882
5327 AA; 607972
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Best Local Similarity 46.4%;
Matches 13; Conservative
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     73
                                                                                                      181
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       VARSPLIC
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Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo
PRINT, FROOTA, HAMP; 1.
SMART; SM00304; HAMP; 1.
SMART; SM00304; HAMP; 1.
SMART; SM0038; HarPase_c; 1.
SMART; SM0038; HisKa, 1.
PROSITE; PS5088; HaMP; 1.
PROSITE; PS50109; HIS KIN; 1.
Complete proteome, Kinase; Phosphorylation; Sensory transduction;
Transferase; Transmembrane.
SEQUENCE 486 AA; 52550 MW; 329BBCC0C94D017C CRC64;
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Homo.
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SEQUENCE FROM N.A. (ISOFORM 2).
SEQUENCE-20001959; PubMed=10529403; DOI=10.1006/bbrc.1999.1538;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 42.9%; Pred. No. 1e+02;
Matches 12; Conservative 6; Mismatches 10; Indels
                                                                                                                                                                                                                                            Query Match 35.6%; Score 69; DB 2; Length 486; Best Local Similarity 41.7%; Pred. No. 6.3; Matches 15; Conservative 7; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4433 AA; 505640 MW; 329C01910D97EE6C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Butheria, Primata, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BAA32310;
02-MRR-2004 (TrEMBLrel. 27, Created)
02-MRR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                           209 PVGRSGDELDRLAENLNAMLERIEALMAGLKEVSDN 244
                                                                                                                                                                                                                                                                                                                                            5 PVGRDAETLOKOKETIKAFLKKLEALMAS----NDN 36
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Okuda T., Matsuda S., Nakatsugawa S., Ichigotani Y., Iwahashi N., Takahashi M., Ishigaki T., Hamaguchi M.; "Molecular cloning of macrophin, a human homologue of Drosophila kakapo with a close structural similarity to plectin and dystrophin.";
                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).

SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=20026884; PubMed=10559337;

Sun Y., Zhang J., Kraeft S.-K., Auclair D., Chang M.-S., Liu Y.,

Sutherland R., Salgia R., Griffin J.D., Ferland L.H., Chen L.B.;

Molecular cloning and characterization of human trabeculin-alpha, a giant protein defining a new family of actin-binding proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIŜSUE=Brain;
MEDLIRE=22158633; PubMed=12168954;
Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
"Construction of expression-ready cDNA clones for KIAA genes: manual
curation of 330 KIAA cDNA clones.";
DNA Res. 9:99-106(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-98116662; PubNed=9455484;
Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,
Nakajima D., Nomura N., Ohara O.;
Nakajima D., Nomura N., Ohara O.;
"Characterization of CDNA clones in size-fractionated cDNA libraries
from human brain.";
DNA Res. 4:345-340(1997)
-I-FUNCTION: F-actin-binding protein which may play a role in cross-
linking actin to other cytoskeletal proteins. Also binds to
microtubules (By similarity).
-I-SUBCELLULAR LOCATION: Cytoplasmic.
-I-ALTERNATIVE PRODUCTS:
EVENT ALTERNATIVE PRODUCTS:
EVENT ALT
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"Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 6:337-345(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=20039619; PubMed=10574462;
Nagase T., Ishikawa K.-I., Kikuno R., Hirosawa M., Nomura N.,
                                                                                                                                                                                                                                                                                                                                           -1 TISSUE SPECIFICITY: Ubiquitcusly expressed.
-1 TISSUE SPECIFICITY: Ubiquitcusly expressed.
-1 SIMILARITY: Belongs to the plakin or cytolinker family.
-1 SIMILARITY: Contains 1 actin-binding domain.
-1 SIMILARITY: Contains 2 calponin-homology (CH) domains.
-1 SIMILARITY: Contains 2 FP-hand calcium-binding domains.
-1 SIMILARITY: Contains 1 SH3 domain.
-1 SIMILARITY: Contains 37 spectrin repeats.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corby N.; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lsoId=Q9UPN3-3; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=Q9UPN3-1; Sequence=VSP_007341;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=2;
IsoId=Q9UPN3-2; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [7]
SEQUENCE OF 3734-5430 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [5]
SEQUENCE OF 1544-5057 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 868-2350 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Brain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=4;
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the European Bioinformatics Institute. There are no restrictions on its
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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                                                                                    TISSUE SPECIFICITY: Expressed in heart, lung, pituitary and placenta, not found in brain, kidney, liver, pancreas or skeletal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Calcium-binding; Coiled coil;
                                                                                                                    -!- SIMILARITY: Belongs to the plakin or cytolinker family.
-!- SIMILARITY: Contains 2 EF-hand calcium-binding domains.
-!- SIMILARITY: Contains 19 plectin repeats.
-!- SIMILARITY: Contains 32 spectrin repeats.
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EMBL; AF325341; AAL38997.1; ---
EMBL; AF325333; AAL38997.1; ---
EMBL; AF325333; AAL38997.1; JOINED.
EMBL; AF325335; AAL38997.1; JOINED.
EMBL; AF325336; AAL38997.1; JOINED.
EMBL; AF325339; FAL38997.1; JOINED.
EMBL; AF325339; FAL38997.1; JOINED.
EMBL; AF325339; FAL38997.1; JOINED.
EMBL; AF325339; FAL38997.1; JOINED.
EMBL; AF325339; FC.CTCONGED.
EMBL; AF325339; FC.CTCONGED.
EMBL; AF32539; FC.CTCONGED.
EMBL; AF325339; FC.CTCONGED.
EMBL; AF325339; FC.CTCONGED.
EMBL; AF325339; ABCCONGED.
EMBL; ALCENATIVE SPORTER.
EMBL; AF325339; ABCCONGED.
EMBL; AF32539; ABCCONGED.
EMBL; AF3253997.1; JOINED.
EMBL; AF325397.1; JOINED.
EMBL; AFA35707.1; JOINED.
EMBL; AF325707.1; JOINED.
EMBL; AF3257.1; JOINED.
EMBL; AF3257.1; JOINED.
EMBL; AF3257.1; JOINED.
EMBL; AF325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IsoId=096PK2-1; Sequence=Displayed;
                    Name=1;
IsoId=Q9UPN3-1; Sequence=External;
                                           Name=2;
IsoId=Q9UPN3-2; Sequence=External;
                                                                            IsoId=Q9UPN3-3; Sequence=External;
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3322341932
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3319323
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Pred. No. 1.3e+02;
6; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAC4 HUMAN STANDARD; PRT; 5938 AA.
Q96PKZ; Q8WXY;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
Microtubule-actin crosslinking factor 1, isoform 4.
Mame=MACFI; Synonyms=ACF7, ABP620, KIAA0465, KIAA1251;
Homo sapiens (Human).
                     (Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
(Potential).
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3083 MGAIGRDIDSLQSQIEDVRLFLNKIHVL 3110
Coiled coil (Coiled coil (Spectrin 1.) Spectrin 3.) Spectrin 3.
                                                                                                                                                                                                                                                                                                                                                                                          Spectrin 24.
Spectrin 25.
Spectrin 26.
Spectrin 27.
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                                                                                                                                                                                 Spectrin 6.
Spectrin 7.
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Spectrin 9.
Spectrin 10
Spectrin 11
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Spectrin 1
Spectrin 2
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Best Local Similarity 42.9%;
Matches 12; Conservative
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115342
115342
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22040
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MAC4_HUMAN
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REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE FROM N.A.

REQUENCE TO NOTE 10.1038 Unbeg23;

REALN=CGA009 / ATCC BAA-98;

RADMOGL=1704707; DOI=10.1038 Unbeg21;

RADMOGL=1704707; DOI=10.1038 Unbeg21;

RADMOGL=1704707; DOI=10.1038 Unbeg21;

RADMOGL=1704707; DOI=10.1038 Unbeg C., Torres y Torres J.L., Peres C.,

RADMOGL=1704 RADMOGL=1. Reatty J.T., Lang A.S., Tabita F.R.,

RADMOGNATHHELD bacterium Rhodopseudomonas palustris.";

RATE BACCELULAR LOCATION: Integral membrane protein (By similarity).

- I SUMICHARITY: Contains I histidine kinase domain.

REMBL; BX572599; CAR27373.1;

- I SIMILARITY: Contains I histidine kinase domain.

REMBL; BX572599; CAR27373.1;

- I SIMILARITY: Contains I histidine kinase domain.

REPERO; IPRO03569; HAMP.

RICEPRO; IPRO03569; HAMP.

RICEPRO; IPRO03661; His kinase.

RICEPRO; ROO0367; HAMP; I.

REAM; PRO0319; HAMP; I.

SNART; SMO0389; HAMP; I.

SNART; SMO0389; HAMP; I.

SNART; SMO0389; HAMP; I.

RECOURTE: PSSO088; HAMP; I.

RECOURTE: PSSO089; HAMP; I.

RECOURTE: PSSO089; HAMP; I.

RECOURTE: PSSO088; HAMP; I.

RECOURTE: PSSO089; HAMP; I.
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Land M.L., Pelletier D.A., Beatty J.T., Lang A.S., Tabita F.R.,
                                                                                                                                                                                             Rhodopseudomonas palustris.
Barteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Bradyrhizobiaceae, Rhodopseudomonas.
VCB__TaxID=1076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EPA1932.
Rhodopseudomonas palustris.
Rhodopseudomonas palustris, Proteobacteria; Rhizobiales;
Bradyrhizobiaceae; Rhodopseudomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.0%; Score 66; DB 2; Length 482; 38.9%; Pred. No. 15; ive 8; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE 482 AA; 52144 MW; F1D1055E1D0975D3 CRC64;
                                    Created)
Last sequence update)
Last annotation update)
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02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
Sensor histidine kinase precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 PVGRDAETLQKQKETIKAFLKKLEALMAS----NDN 36
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                                       05-JUL-2004 (TrEMBLrel. 27, Created 05-JUL-2004 (TrEMBLrel. 27, Last se 05-JUL-2004 (TrEMBLrel. 27, Last se Sensor histidine kinase precursor. OrderedLocusNames=RPA1932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transmembrane.
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STRAIN=CGA009 / ATCC BAA-98;
PubMed=14704707;
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SIGNAL 1
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Matches 14; Conserv
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CAE27373;
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Pred. No. 1.4e+02;
6; Mismatches 10; Indels
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670134 MW; B8784112752DA004 CRC64;
Coiled coil (Potential).
Coiled coil (Potential).
Coiled coil (Potential).
Coiled coil (Potential).
Coiled coil (Potential).
EF-hand 1 (Potential).
EF-hand 2 (Potential).
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Spectrin 5.
Spectrin 6.
Spectrin 7.
Spectrin 8.
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Plectin 3.
Plectin 3.
Plectin 5.
Plectin 6.
Plectin 7.
Plectin 10.
Plectin 11.
Plectin 12.
Plectin 13.
Plectin 14.
Plectin 14.
Plectin 15.
Plectin 16.
Plectin 17.
Plectin 17.
Plectin 17.
Plectin 17.
Plectin 18.
Spectrin 17.
Spectrin 18.
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Spectrin 32.
P -> S (in R
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Spectrin 1
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Spectrin 1
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Spectrin 2
Spectrin 2
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Spectrin 2
Spectrin 2
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Spectrin 2
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Best Local Similarity 42.9
Matches 12; Conservative
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11158
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11196
2032
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EMBL; AB076670; BAC00814.1; -.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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   Torres y Torres J.L., Peres C.,
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MEDLINE=20181125; PubMed=10718197;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Kotani H.,
Tabata S.;
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34.0%; Score 66; DB 2; Length 649;
Best Local Similarity 37.5%; Pred. No. 20;
Matches 15; Conservative 9; Mismatches 8; Indels
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34.0%; Score 66; DB 2; Length 482;
Best Local Similarity 38.9%; Pred. No. 15;
Matches 14; Conservative 8; Mismatches 10; Indels
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Gibson J.L., Hanson T.E., Bobst C., Torres y Torres J.L.,
Harrison F.H., Gibson J., Harwood C.S.;
"Complete genome sequence of the metabolically versatile
photosynthetic bacterium Rhodopseudomonas palustris.";
Nat. Biotechnol. 22:55-61 (2004).
EMBL; BX572599; CAE27373.1;
Kinase; Signal.
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clones."; 31-63(2000).
DNA Res. 7:31-63(2000).
EMBL; AB018120; BAA97285.1; -.
Interro; IPR008545; DUF827.
Fram; PR05701; DUF827; 1.
Pram; PR05701; DUF827; 1.
Res. 72430 MW; B7D51EFB295D55BB CRC64; Man, PR051EFB295D55BB CRC64; Man, PR051EFB
                                                                                                                                                                                                                             33 Potential.
52144 MW; F1D1055E1D0975D3 CRC64;
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-007-2003 (TrEMBLrel. 25, Last annotation update)
Myosin heavy chain-like.
Arabidopsis thaliana (Mouse-ear cress).
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 12
Q9LVQ4
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TISSUBBLEAR CANCEY,

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

KIAUSDET R.D., Collins F.S., Wagner L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Heigh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Carainci P., Prange C.,

Bromstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.S., Worley K.C., Hale S., Garcia A.M. Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M. X., Gibbs R.A.,

Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

A Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Mederger D.M., Schein J.E., Jones S.J.M., Marra M.A.,

"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=CS7BL/60; TISSUB=Brain, and Embryo; MEDINELS2584683; Dubmed=1246681; DOI=10.1038/nature01266; MEDINE=22354683; Pubmed=1246681; DOI=10.1038/nature011.0 Structo M., Saito R., Adachi J., Bono H., Kondo S., Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Golobori T. Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schrin L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCC2 MOUSE STANDARD; PRT; 1679 AA.
Q8CHG3; QBR44; QBR2Q5; Q9CH45;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 44, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
GRIP and colled-coil domain-containing protein 2 (Golgi coiled coil
protein GCCL85).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=Gcc2; Synonyms=Kiaa0336;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 PVGRDAETLOKOKETIK-----AFLKKLEALMASNDNANKT 40
GO; GO:0016020; C:membrane; IEA.
GO; GO:0008565; F:protein transporter activity; IEA.
GO; GO:0006886; P:intracellular protein transport; IEA.
                                                                                                                                                                                                                                                                 PEGM; PF05739; SNARE; I.
PEGM; PF00804; SYNTAXIN; 1.
SWART; SM00397; L.SNARE; 1.
PR0STITE; PS00144; SYNTAXIN; 1.
PR0STITE; PS50192; T. SNARE; 1.
SEQUENCE 286 AA; 33028 MW; 5FBID6BI0B77DEAB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 65.5; DB 2; I
Pred. No. 10;
6; Mismatches 13;
                                                                                                                InterPro; IPR006012; Syntaxin.
InterPro; IPR006011; Syntaxin.N.
InterPro; IPR010999; t-snare.
InterPro; IPR000727; T_SNARE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33.8%;
39.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-769 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-442 FROM N.A.
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Best Local Similarity
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RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Balake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Gagard T., Gariboldi M., Gissi C., Godzik A., Gough J., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Ranai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Konagaya A., Kurochkin I.V., Lee Y., Lehard B.L., Mith H., Maltais L., Marchianni L., McKenzie L., Miki H., Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G., Percosky, N., Pillaia R., Pontius J.U., Oil, Ramadandran S., Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M., Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K., Schneider C., Semple C.A., Setou M., Shimada K., Sthiana E., Wahlest C., Wahlest C., Watanabe Y., Walls C., Wallan B.C., Wandle C.A., Setou M., Shimada K., Sthiming L.G., Wynshaw-Boris A., Yanagisawa M., Sakazume N., Saxolan N., Zavolan M., Sakazume N., Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22579201; PubMed=12693553; MEDLINE=22579201; PubMed=12693553; MEDLINE=22579201; PubMed=12693553; MEDLINE=22579201; PubMed=12693553; Makajima D., Ndyase T., Ohara N., Noga H.; Wakajima D., Ndyase T., Ohara O., Koga H.; Mouse homologues of KIAA gene: II. The complete nucleotide sequences of 400 mouse KIAA-homologous connections identified by screening of terminal sequences of cDNA clones andomly sampled from size-fractionated libraries."; DNA Res. 10:35-48(2003).
-!- FUNCTION: Probably involved in maintaining Golgi structure (By

similarity).
SUBCELLULAR LOCATION: Cytoplasmic; peripheral membrane protein associated with the trans-Golgi network (by similarity).
DOMAIN: Extended rod-like protein with coiled-coil domains.
SIMILARITY: Belongs to the golgin family.
SIMILARITY: Contains 1 GRIP domain.

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Glu-rich.
GRID.
I -> M (in Ref. 2).
WW. 6E2P84263E5E0103 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; BC027339; AAH27339.1; ALT_INIT.
EMBL; AX01206; BAB27466.2; --
EMBL; AX045701; BAC32463.1; --
EMBL; AB093222; BAC41416.1; --
PIR; PT0649; PT0712.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP, P05554, 1NWQ.
MGD; MGI:1917547, 2600014C01Rik.
InterPro; IPR002037; GRIP.
InterPro; IPR002017; Spectrin.
Ffam; PF01465; GRIP; 1.
PROSITE; PS50913; GRIP; 1.
Coiled coil; GQIgi stack.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1679 AA; 194443 MW;
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STRAIN-ATCC 19718 / IFO 14298;

STRAIN-ATCC 19718 / IFO 14298;

STRAIN-ATCC 19718 / IFO 14298;

STRAIN-ATCC 19718 / IFO 14298;

STRAIN-ATCC 19718 / IFO 14298;

STRAIN-ATCC 19718 / IED TO 14298;

STRAIN-ATCC 19718 / IED TO 14298;

STRAIN-BEED SEGGIO FUNDED TO 15, Sayavedra-Soto L.A.,

Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,

A Arcibero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

A Arcibero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

A Arcibero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

A Arcibero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;

A Complete genome sequence of the amonomia-oxidizing bacterium and

ST. STRIILARITY: Belongs to the ABC transporter family.

STRIIL BX321857; CAD84388.1; -

CO GO:0005224; Frap binding casestte (ABC) transporter acti...; IEA.

GO; GO:000106; Fransport; IEA.

GO; GO:000106; Fransporter; IEA.

InterPro; IPR003439; ABA ATPase.

InterPro; ABA ATPASE.

InterPro; IPR003439; ABA ATPASE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nitrosomonas europaea.
Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
Nitrosomonadaceae; Nitrosomonas.
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUR-2004 (TrEMBLrel. 26, Last annotation update)
ATPase components of ABC transporters with duplicated ATPase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 33.5%; Score 65; DB 2; Length 636; Best Local Similarity 36.4%; Pred. No. 26; Matches 12; Conservative 11; Mismatches 10; Indels
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PROSITE; PS50893; AEC_TRANSPORTER_2; 2.
ATP-binding; Complete profes
SEQUENCE 636 AA; 71849 MW; 2C822331AECA0288 CRC64;
                                             4 APVGRDAETLQKQ----KETIKAFLKKLEALMASNDNANK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   587
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                                                                                                                                                                                                                                                                                                                                636 AA
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                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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Gaps

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14; DB 1;

Score 65.5; DB: Pred. No. 59; 6; Mismatches

Query Match
Best Local Similarity 39.0%;
Matches 16; Conservative

Length 1679; Indels

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FEATURE
8001064666666444444
8001064666666444444
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Sequence 4, Appli
                                                                                                                           November 10, 2004, 13:44:14 ; Search time 12.0792 Seconds (without alignments) 181.178 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1. /cgn2 6/ptodata1/liaa/5A_COMB.pep:*

2. /cgn2 6/ptodata1/liaa/6A_COMB.pep:*

3. /cgn2 6/ptodata1/liaa/6A_COMB.pep:*

3. /cgn2 6/ptodata1/liaa/6B_COMB.pep:*

5. /cgn2 6/ptodata1/liaa/PCTUS COMB.pep:*

5. /cgn2 6/ptodata1/liaa/Packfiles1.pep:*
                 GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-134-000C-4180

US-09-248-796A-24252

US-09-107-532A-5265

US-09-107-532A-5265

US-09-100-040-3

US-09-000-040-3

US-09-000-041-2

US-09-252-991A-28655

US-09-252-991A-28655

US-09-252-991A-28655

US-09-252-991A-28655

US-09-252-991A-28655

US-09-252-991A-28655

US-09-252-991A-28655

US-09-242-6483

US-09-248-166A-483

US-09-248-166A-483

US-09-248-166A-483

US-09-248-196A-15247

US-08-442-063A-45

US-08-442-063A-45

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162
1 CREQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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                                                                                                                                                                                                                                                                                                                                    478139 segs, 66318000 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                         - protein search, using sw model
                                                                                                                                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                           Minimum DB seq length: 0 . Maximum DB seq length: 2000000000
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Match 1
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                                                                                                                                                                                                                                                                                Scoring table:
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48.5
47.4
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                                                                                                                                                                                                                                            Sequence:
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No.
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Patent No. 655195

GENERAL INFORMATION:

APPLICANT:

MATC J. Rubenfield et al.

APPLICANT:

TITLE OF INVENTION:

TITLE OF INVENTION:

ARUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

TOTOBE REPRESENCE:

107196.136

CURRENT APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR PLING DATE: 1998-07-21

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 30269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
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APPLICANT LYMN DOUGETTE-Stamm et al

APPLICANT LYMN DOUGETTE-C ACID AND AMINO ACID SEQUENCES RELATING TO

TITLE OF INVENTION: BUTEROCCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 032796-032

CURRENT APPLICATION NUMBER: US/09/134,000C

CURRENT PILING DATE: 1998-08-13

PRIOR FILING DATE: 1997-08-15

NUMBER OF SEQ ID NOS: 6812

SSECTIAND AND SECUENCE ACID NOS: 6812

SSECTIAND ALBORIN VERSION 3.1

ENGTH: 178

LENGTH: 178
                                                  Gaps
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Query Match
35.2%; Score 57; DB 4; Length 248;
Best Local Similarity 37.5%; Pred. No. 0.33;
Matches 12; Conservative 8; Mismatches 12; Indels
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34.6%; Score 56; DB 4;
Best Local Similarity 35.5%; Pred. No. 0.32;
Matches 11; Conservative 10; Mismatches
                                                                                             2 REQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
                                                                                                                              3 EQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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                                                                                                                                                                                                                                         US-09-134-000C-4180
; Sequence 4180, Application US/09134000C
; Patent No. 6617156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , ORGANISM: Enterococcus faecalis
US-09-134-000C-4180
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US-09-252-991A-30269
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RESULT 4 US-09-248-796A-24252

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Sequence 24552, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
MOTION WELL OF INVENTION:
MOTION:
MOTION FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFRENCE:
MOTION 1099-02-12
CURRENT APPLICATION NUMBER:
US 60/074,725
PRIOR PILING DATE:
MOMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5265, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .
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CORRESPONDENCE ADDRESSES
ADDRESSEE: GENOME THEAPEUTICS CORPORATION
STREET: 100 Beaver Street
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MEDIUM TYPE: CD/ROM ISO9660
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31.5%; Score 51; DB
Best Local Similarity 24.1%; Pred. No. 0.9;
Matches 7; Conservative 11; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 EQAELTGLRLASLGLKFNKIVHSSMTRAI 31
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INFORMATION FOR SEQ ID NO: 5265:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JS-09-248-796A-24252
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APPLICANT: Law, Joseph S.
APPLICANT: Burrows, Lori
APPLICANT: Burrows, Lori
APPLICANT: Burrows, Lori
APPLICANT: Charter, Debox
APPLICANT: Charter, Debox
APPLICANT: Charter, Debox
TITLE OF INVENTION: No. 5994072el Proteins Involved in the Synthesis and Assembly
TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
TITLE OF INVENTION: Of O-Antigen in Pseudomonas Aeruginosa
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 2.0
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                                          Gaps
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  Length 355;
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                                            Indels
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  DB 3;
Query Match 29.9%; Score 48.5; I Best Local Similarity 44.8%; Pred. No. 12; Matches 13; Conservative 7; Mismatches
                                                                                                          271 AIVTNVRMSPVELNQFAKQVHSSMHRGIQ 299
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                                                                                 5 AELTGLRLASLGL-KFNKIVHSSMTRAIE 32
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; Sequence 9, Application US/08846762A
Patent No. 5994072
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 LRLASLGLKFNKIVHSSMT 28
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TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 57.9
Matches 11; Conservative
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LENGTH: 316
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Batent No. 6562958

GRNERAL INFORMATION:

APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BADWANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GTC99-03PA

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 6664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09000040B

Sequence 3, Application US/09000040B

Patent No. 6180388

GENERAL INFORMATION:
APPLICANT: FROUZET, Didier

APPLICANT: FAVEE-BUllE, Olivier
APPLICANT: FAVEE-BUllE, Olivier
APPLICANT: PETRE, Dominique
APPLICANT: PIERRARD, Jerome
APPLICANT: PIERRARD, Jerome
APPLICANT: PIERRARD, Jerome
APPLICANT: PIERRARD, Jerome
APPLICANT: FIREARD, Jerome
APPLICANT: PIERRARD, Jerome
APPLICANT: GUITTON, Carole
TITLE OF INVENTION: HYDROLYSE POLYAMIDES
TITLE OF INVENTION: HYDROLYSE POLYAMIDES
TITLE OF INVENTION: HYDROLYSE POLYAMIDES
TITLE OF INVENTION: HYDROLYSE POLYAMIDES
TILLE OF TOWNERT: CB 956-035
CURRENT APPLICATION NUMBER: US/09/000,040B
CURRENT APPLICATION NUMBER: FP 95/08917
EARLIER FILING DATE: 1995-07-18
EARLIER FILING DATE: 1995-07-18
EARLIER FILING DATE: 1995-07-17
NUMBER OF SEQ ID NOS: 4
SOSTWARRE PATENTING OF 12
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31.5%; Score 51; DB 4; Le
Best Local Similarity 35.5%; Pred. No. 3;
Matches 11; Conservative 9; Mismatches 11;
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48 EEAKEGGRKIKEAGIEFDVAYTSVLTRAIKT 78
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29.9%; Score 48.5; D
Best Local Similarity 53.6%; Pred. No. 3.3;
Matches 15; Conservative 3; Mismatches
                                          NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...242
SEQUENCE DESCRIPTION: SEQ ID NO: 5265:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 ABLTG-LRLASLGLKFNKIVHSSMTRAI 31
    ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT; ORGANISM: Acinetobacter baumannii
US-09-328-352-6864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Comamonas acidovorans
US-09-000-040-3
                                                                                                        US-09-107-532A-5265
                          FEATURE
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Gaps

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APPLICANT: Mitcham, Consider L.
APPLICANT: Mitcham, Consider L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Harlocker, Susan Louise
APPLICANT: Walos Yuqui
APPLICANT: Read, Stewn G.
APPLICANT: Reter, Mark
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APPLICANT: Reter, Mark
APPLICANT: Reter, Mark
APPLICANT: Rolk, John
APPLICANT: Bolk, John
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                        APPLICANT: Makowski, Lee
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Hyman, Paul
APPLICANT: Holiams Mark
TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES
FILE REPERENCE: 8471-010-999
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT APPLICATION NUMBER: US/09/914,259
CURRENT APPLICATION NOT: 180
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
IENOTH: 540
TYPE: TENOTH: 540
TYPE: TO 30
CREANISM: Caenorhabditis elegans
US-09-914-259-30
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Patent No. 6620922
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Davin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan Louise
APPLICANT: Reed, Steven G.
APPLICANT: Redo, Michael
APPLICANT: Renger, Gary
APPLICANT: Retner, Mark
APPLICANT: Solk, John
APPLICANT: Solk, John
APPLICANT: Bolk, John
APPLICANT: Day, Craig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 483, Application US/09439313
Patent No. 6329505
GENERAL INFORMATION:
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                                                                                                                                                      Sequence 20001, Application US/09252991A

Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US 60/094,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PELING DATE: 1998-02-18
PRIOR PELING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 20001
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Patent No. 6551795

GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

SEQ ID NO 28655

LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: Identity of amino acid at the above locations are unknown. US-09-252-991A-20001
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359 ALLSGERLASLGLKKGOKVIASFDPA 384
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US-09-914-259-30
Sequence 30, Application US/09914259
Parent No. 6499336
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116 LAVASLGLGINKLVLSLLT 134
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-28655
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Pseudomonas aeruginosa
FEATURE:
                                                                                                         RESULT 10
US-09-252-991A-20001
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US-09-252-991A-28655
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Gaps

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                                                                                            APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Stolk, John A.
APPLICANT: Day, Craig H.
APPLICANT: Carter, Darrick
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wedy, Yasir A.W.
APPLICANT: Wedy, Yasir A.W.
APPLICANT: Welky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
FILE REFERENCE: 210121.42717C17
CURRENT FAPLICATION NUMBER: US/09/636,215
CURRENT FILING DATE: 2000-08-10
NUMBER OF SEQ ID NOS: 852
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 483
LENGTH: 143
TYPE: PRT
ORGANISM: Homo sapiens
US-09-636-215-483
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APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Kalos, Michael D.
APPLICANT: Retter, Mary M.
APPLICANT: Stolk John A.
APPLICANT: Stolk John A.
APPLICANT: Order, Thomas S.
APPLICANT: Li, Samuel
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Wang, Milliam
APPLICANT: Wang, Milliam
APPLICANT: Hepler, William
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53 CRKQPKLPSMRLSLLWPWRDLKFVPRQDKLTRSSVSVA 90
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US-09-685-166A-483
S-09-685-166A-483
Sequence 483, Application US/09685166A
Pacent No. 6630305
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqui
APPLICANT: Handerson, Robert A.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stolk, John A.
APPLICANT: Carter, John A.
APPLICANT: Carter, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Lay, Samuel
Henderson, Robert A.
Kalos, Michael D.
                                                                              Fanger, Gary R.
Retter, Marc W.
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ORGANISM: Homo sapiens
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November 11, 2004, 01:28:30; Search time 38.1679 Seconds (without alignments) 305.399 Million cell updates/sec GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 162 1 CREQAELTGLRLASLGLKFNKIVHSSMTRAIET 33 Total number of hits satisfying chosen parameters: 1566620 segs, 353225886 residues Post-processing: Minimum Match .0% Maximum Match 100% Listing first 45 summaries - protein search, using sw model BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 US-10-092-750-53 Scoring table: Perfect score: OM protein Sequence: Searched: Run on:

Published Applications AA:*

| Can2 6/ptodata1/pubpaa/US07 PUBCONB.pep:*
| Can2 6/ptodata1/pubpaa/US07 PUBCONB.pep:*
| Can2 6/ptodata1/pubpaa/US06 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/US06 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/US07 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/US08 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/US08 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/US08 NBW PUB.pep:*
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| Can2 6/ptodata1/pubpaa/US106 PUBCOMB.pep:*
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| Can2 6/ptodata1/pubpaa/US10B PUBCOMB.pep:*
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| Can2 6/ptodata1/pubpaa/US10B PUBCOMB.pep:*
| Can2 6/ptodata1/pubpaa/US10B PUBCOMB.pep:*
| Can2 6/ptodata1/pubpaa/US11 NBW PUB.pep:*
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| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
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| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*
| Can2 6/ptodata1/pubpaa/USS0 NBW PUB.pep:*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		53, Appl	1843, Ap	263315,	147607,	147651,		726, App	162719,	198729,	11212, A	2284, Ap	53813, A	147640,
	Description	Sequence 53, Appl	Seguence	Sequence 263315,	Sequence 147607,	Sequence	Seguence	Seguence	Seguence	Sequence	Sequence	Seguence	Seguence	Seguence
	QI	US-10-092-750-53	US-10-408-765A-1843	US-10-424-599-263315	US-10-437-963-147607	US-10-437-963-147651	US-10-425-114-36853	US-10-310-154-726	US-10-437-963-162719	US-10-424-599-198729	US-10-369-493-11212	US-10-369-493-2284	US-10-282-122A-53813	US-10-437-963-147640
	,	14	16	15	16	16	15	14	16	15	14	14	15	16
	Match Length DB	33	255	121	1059	1112	258	511	205	378	307	211	444	1299
ا ا	Match	100.0	94.4	35.8	35.8	35.8	35.2	35.2	33.3	32.1	31.8	31.5	31.5	31.5
	Score	162	153	80	28	58	57	57	54	52	51.5	21	51	51
1	No.	П	7	m	4	ហ	9	7	œ	6	10	11	12	13

Sequence 13404, A	Sequence 12082, A	Sequence 4610, Ap	Sequence 7367, Ap	Seguence 164742,	Sequence 60021, A	Sequence 316, App	Sequence 65105, A	Sequence 273644,	Sequence 7903, Ap	Sequence 231231,	Sequence 62748, A	Sequence 231230,	Sequence 329406,	Sequence 16966, A	Sequence 176174,	Sequence 64344, A	Sequence 34, Appl	Sequence 276160,	Sequence 2578, Ap	Sequence 276161,	Sequence 203921,	Sequence 1088, Ap	Sequence 199176,	Sequence 185, App	ر م	Seguence 63861	ΑÞ	4344]	855,	equence 30,	119,
-156-761-134	-369-493-1	-369-493	-369-493	-424-599	-425-114	-369-493	-425-114	-425-115	-739-930	-425-11	-425-114	-425-115	-425-115	-369-493	-437-963	-425-114	-221-625	US-10-425-115-276160	-094-749	-425-115	-425-115	-369-493	-437-963	-369-490	-216-209-	-282-122A-6	815-24	-282-122A-4	-112-944-85	-080-608A-3	-370-68
14	14	14	14	15	15	14	13	17	17	17	15	17	17	14	16	15	15	17	14	17	17	14	16	14	14	13	σ		15	14	14
438	206	223	223	268	308	311	654	815	992	00	1030	90	57	237	261	505	834	848	850	869	115	306	1525	311	316	320	411	411	441	540	540
31.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	30.2	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.6	29.3	29.3	29.3	29.0	29.0	29.0	29.0	29.0	29.0	29.0	29.0
50.5	4	49	49	49	49	9	40	4.0	4	4	40	4	48	48	48	48	48	. 48	48	48	7	7	47.5	47	47	47	47	47	47	47	47
14	15	16	17	18	19	50	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	. 43	44	45

## ALIGNMENTS

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US-10-092-750-53

Sequence 53, Application US/10092750

Publication No. US20030032157A1

GENERAL INFORMATION:
Publication No. US20030032157A1

GENERAL INFORMATION:
Publication No. US2003003157A1

APPLICANT: Wright, Martin C.
TITLE OF INVENTION: Polypeptides Interactive with BCL-X1

FILE REFERENCE: 50036/050002

CURRENT APPLICATION NUMBER: US/10/092,750

CURRENT FILING DATE: 2002-03-08

NUMBER OF SEQ ID NOS: 253

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 53

LENGTH: 33

TYPE: RRT

OUETY MATCH

GUEST MATCH

Best Local Similarity 100.0%; Pred. No. 2.1e-17;

Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps

Qy

1 CREOALIGISMIRASININININES: 33
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RESULT 2
US-10-408-765A-1843
Sequence 1843, Application US/10408765A
Publication No. US20040101874A1
GENERAL INFORMATION:

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NAME/KEY: unsure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: La ROSa Thomas J
APPLICANT: La ROSa Thomas J
APPLICANT: Exovalic David K
APPLICANT: About Shua
APPLICANT: About Shua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPREBENCE: 38-21 (53223) B
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
SUMRENT FILING DATE: 2003-04-28
SEQ ID NOS: 285684
SEQ ID NO. 263315
LENGTH: 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                     APPLICANT: Zhang, Bing
APPLICANT: Zhang, Bing
APPLICANT: Glann, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glenn, Gary M.
APPLICANT: Warnock, Dales F.
TITLE OF INVENTION: TAKGETS F.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
TITLE OF INVENTION: 10089.465
CURRENT APPLICATION UNBER: US/10/408,765A
CURRENT APPLICATION UNBER: US/10/408,765A
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 1843
LENGTH: 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: Clone ID: PAT_MRT3847_79796C.1.pep
US-10-424-599-263315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 94.4%; Score 153; DB 16; Bet Local Smilarity 100.0%; Pred. No. 5.6e-15; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
35.8%; Score 58; DB 15;
Best Local Similarity 43.3%; Pred. No. 0.86;
Matches 13; Conservative 5; Mismatches 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        125 REGAELTGLRLASLGLKFNKIVHSSMTRAIET 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 REQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovallic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Ro, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 263315, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
Soumitra S.
Eoin D.
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens US-10-408-765A-1843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 3
US-10-424-599-263315
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APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERBACE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147607
LENGTH: 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: La Rosa, Thomas J.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Excellic, David K.
APPLICANT: Excellic, David K.
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Barbazuk, Brad
APPLICANT: Barbazuk, Brad
APPLICANT: Branch Rosa Nucleic Acid Molecules and Other Molecules Associated With
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147651
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1059;
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                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Clone ID: PAT_MRT4530_4811C.1.pep
US-10-437-963-147607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_4815C.1.pep
US-10-437-963-147651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 35.8%; Score 58; DB 16; Best Local Similarity 43.8%; Pred. No. 11; Matches 14; Conservative 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.8%; Score 58; DB 16; Best Local Similarity 43.8%; Pred. No. 12; Matches 14; Conservative 6; Mismatches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (1)..(1112)
OTHER INFORMATION: unsure at all Xaa locations
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CREQA--ELIGLRLASLGLKFNKIVHSSMTRA 30
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; Sequence 147651, Application US/10437963

; Publication No. US20040123343A1

; GENERAL INFORMATION:
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Sequence 36653, Application US/10425114
Publication No. US20040034888A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihuu
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa
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TYPE: PRT
ORGANISM: Oryza sativa
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CORGANISM: Glycine max
US-10-310-154-726
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Best Local Similarity
Matches 12; Conserv
                                                                                                                                                                                                                                                                                                                                                                                         8
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313) B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 38853
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0
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                                                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700749341_FLI.pep
US-10-425-114-36853
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US-10-310-154-26

Sequence 726, Application US/10310154

Sequence 726, Application US/10310154

Sequence 726, Application US/10310154

GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Adams, Thomas H
APPLICANT: Adams, Thomas G
APPLICANT: Adams, Thomas G
APPLICANT: Annens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Ball, Gin
APPLICANT: Bell, Ein
APPLICANT: Bell, Ein
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deikman, Jill
APPLICANT: Deikman, Jill
APPLICANT: Deikman, Molian
APPLICANT: Deng, Molian
APPLICANT: Deng, Molian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Madson, Linda L.
Malloy, Kathleen A.
McKiel, Christine L.
Miller, Philip W.
Padmayathi, Manchikanti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Dong, Jinzhuo
Dong, Jinzhuo
Duff, Stephen M.
Galligan, Meghan M.
Hinchey, Brenda S.
Huang, Shihshieh
Johnson, G. Richard
Jung, Vincent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Parnell, Laurence D.
Start, William G.
Fennesen, Dan
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Laccetti, Lucille B.
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Luethy, Michael M.
Lund, Adrian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lai, Chao-Qiang
Lee, Gary
Lin, Jie-Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yang, Chunzhi
Zeng, Xiaoping
Zhang, Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vidya, K.R.
Wang, Haiyun
Xin, Zhanguo
Xu, Nanfei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  iu, Jingdong
                                                                                                                                                                                           TYPE: PRT ORGANISM: Glycine max FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT:
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Sequence 162719

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US-10-424-599-198729
US-10-424-599-198729
Sequence 198729, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION
APPLICANT: La Rosa Thomas J
APPLICANT: Chou Vibua
APPLICANT: Can Vorshei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FIRE REFERENCE: 38-21(53223)B
CURRENT APPLICATION NUMBER: US/10/424,599
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APPLICANT: Zhao, Yajuan
APPLICANT: Zhou, Li
TITE OF INVENTION: Gene Sequences and Uses Thereof in Plants
FILE REPRENCE: 38-15(52796)B
CURRENT FILING DATE: 2002-12-04
CURRENT PILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,358
PRIOR PILING DATE: 2001-12-04
NUMBER OF SEQ ID NOS: 736
LENGTH: 511
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Best Local Similarity 43.3%; Pred. No. 6.7;
Matches 13; Conservative 5; Mismatches 12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.3%; Score 54; DB 16; Length 205; 38.7%; Pred. No. 6.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_61784C.1.pep
US-10-437-963-162719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 EQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 EQAELTGLRLASLGLKFNKIVHSSMTRAIE 32
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Gaps

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11; Indels

DB 14; Length 211; 20;

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Score 51; DB 1
Pred. No. 20;
7; Mismatches
                                                                                                                                                                                                                                                                                           40 KEAKLGGERLKSRGYKFDIAFTSALQRAQKT 70
                                                                                                                                                                                                                                         3 EQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 53813, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
   ; ORGANISM: Schizosaccharomyces pombe US-10-369-493-2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
                                                                                                        31.5%;
41.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F: Carr, Grant
: Yamamoto, Robert
: Forsyth, R.
nr.,
                                                                                                    Query Match
Best Local Similarity 41.99
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 40.0%
Warches 12; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-10-2,82-122A-53813
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US-10-437-963-147640
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US-10-369-493-2284

; Sequence 2284, Application US/10369493
; Sequence 2284, Application Wo. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cho, Yongwei
; APPLICANT: Glan, Slater, Steven C.
; APPLICANT: Glan, Sarry S.
; APPLICANT: Glan, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
; TITLE OF INVENTION: UNBER: US/10/369,493
; CURRENT APPLICATION NUMBER: US 60/360,039
; PRIOR PLING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 2284
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                       Query Match 32.1%; Score 52; DB 15; Length 378; Best Local Similarity 40.6%; Pred. No. 27; Matches 13; Conservative 8; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                  ) OTHER INFORMATION: Clone ID: PAT_MRT3847_21476C.1.pep
US-10-424-599-198729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 31.8%; Score 51.5; DB 14; Best Local Similarity 44.0%; Pred. No. 26; Matches 11; Conservative 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CREQAELTGLRLASLGLKF-NKIVHSSMTRAI 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 REQAELTGLRLASLG-LKFNKIVHS 25
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 198729
LENGTH: 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Methanosarcina mazei
US-10-369-493-11212
                                                                                                                                 TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                  FEATURE:
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APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REPERENCE: BLITRA,034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
FRICK APPLICATION NUMBER: 60/201,078
PRICK FILING DATE: 2000-03-21
FRICK APPLICATION NUMBER: 60/206,848
FRICK FILING DATE: 2000-05-22
FRICK FILING DATE: 2000-05-26
FRICK PILING DATE: 2000-05-26
FRICK PILING DATE: 2000-09-06
FRICK APPLICATION NUMBER: 60/230,335
FRICK APPLICATION NUMBER: 60/230,335
FRICK APPLICATION NUMBER: 60/24,578
FRICK PILING DATE: 2000-10-23
FRICK FILING DATE: 2000-11-27
FRICK PILING DATE: 2000-11-27
FRICK PILING DATE: 2000-11-27
FRICK APPLICATION NUMBER: 60/25,625
FRICK APPLICATION NUMBER: 60/250,636
FRICK APPLICATION NUMBER: 60/250,636
FRICK APPLICATION NUMBER: 60/260,308
FRICK FILING DATE: 2001-02-09
FRICK APPLICATION NUMBER: 60/260,308
FRICK FILING DATE: 2001-02-09
FRICK APPLICATION NUMBER: 60/260,308
FRICK FILING DATE: 2001-02-06
FRICK APPLICATION NUMBER: 60/260,308
FRICK FILING DATE: 2001-02-16
FRICK FILING DATE: 2001-02-16
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FRICK FILING DATE: 2001-02-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , ORGANISM: Cornyebacterium diptheriae US-10-282-122A-53813
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Slater, Stewen C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369, 493
CURRENT FILING DATE: 2003-02-28
FRIOR FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12082
LENGTH: 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Mismatches
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.l Similarity 36.7%;
11; Conservative 9
     Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Mesorhizobium loti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-369-493-12082
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                                                                                                  APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Zhou, Yihua
APPLICANT: Wei
APPLICANT: Wei
APPLICANT: Bucharuk, Brid
APPLICANT: Bucharuk, Brid
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT PILLING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 147640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 31.5%; Score 51; DB 16; Length 1299; Best Local Similarity 55.0%; Pred. No. 1.7e+02; Matches 11; Conservative 3; Mismatches 6; Indels (
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US-10-437-963-147640
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31.2%; Score 50.5; DB 14;
Best Local Similarity 43.8%; Pred. No. 55;
Matches 14; Conservative 3; Mismatches 14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: ONURA, SATOSHI
APPLICANT: IKEDA, HARUO
APPLICANT: ISHIKAWA, JUN
APPLICANT: BHIKAWA, JUN
APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SHAKAKI, YOSHIUWKI
APPLICANT: HATTORI, MASAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REPERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-05-30
PRIOR PILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
Sequence 147640, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalid, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Boukharov, Andrey A.
APPLICANT: Backharov, Andrey A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13404, Application US/10156761
Publication No. US20030119018A1
GENERAL INFORMATION:
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US-10-369-493-12082
; Sequence 12082, Application US/10369493
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; ORGANISM: Streptomyces avermitilis
US-10-156-761-13404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | :|| ||:|||
| 354 RKKDLYAEFNDIVHNSLTRA 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 RLASLGLKFNKIVHSSMTRA 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Oryza sativa FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-156-761-13404
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November 10, 2004, 13:40:53; Search time 8.09434 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

Title: Perfect score:

US-10-092-750-53 162 1 CREQAELTGLRLASLGLKFNKIVHSSMTRAIET 33 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Minimum DB seq length: 0 Maximum DB seq length: 2000000000

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
1: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ф			SOLITINATES	
		Query	ngth	DB		
		٦.	(CD)	į٥	T12682	hypothetical prote
7	82	0	ø		T16702	_
m		4.	3		S67185	_
4		ά.	φ		AE1834	hypothetical prote
S		ď.	α		T46943	mannopine synthesi
9		N	Э		G83416	
7	52.5		331		G72273	probable dioxygena
œ	52	32.1	N		A64091	phosphoglycerate m
6	52	32.1	N	N	AE1350	phosphoglyceromuta
10	52	α.	N	(1	AH1720	phosphoglyceromuta
11	51.5	ä	g	~	A83508	hypothetical prote
12	21	ä	_	~	843214	phosphoglycerate m
13	50	0	М	0	AF3540	phosphoglycerate m
14	50	。	9	~	A71727	hypothetical prote
15	φ.	ö	0	7	G84564	probable sugar tra
16	48.5	6.	S	7	A47039	O)
17	œ.	6.	1	7	95	preprotein translo
18	48	ο.	9	Н	S74345	phosphohistidine p
19		۷.	N	7	54	phosphoglycerate m
20	48	φ.	3	7	D87529	phosphoglycerate m
21	48	ο.	T)	~	F87259	hypothetical prote
22	48	٩.	9	7	T38420	DNA
23	47.5	σ,	0	N	D64497	aspartate carbamoy
24	47	ο.	S	7	B83584	
25	47	φ.	0	Н	OWSEAC	
26	47	ο,	Н	7	97	aspartate carbamoy
27	47	ο.	S	7	8708	
28	47	29.0	346	7	T10173	ı
29	47	ω.	Н	7	8325	O-antigen transloc

chromosomal replic chromosomal replic kinesin light chai	protein C18C4.10 [ kinesin light chai kinesin light chai	glyceraldenyde-3-p glutamate synthase glycerol-3-phospha	pantoate beta-alan hypothetical prote hypothetical prote	aspartate carbamoy L-selectin precurs	ď
D97814 C71665 S41865	H89052 S41864 S47997	C96497 F82085 D64090	F90066 C86011 C91165	AD1059 S22124	744155
01 01 01	0 0 0	0 0 0	0 0 0	01 01 01	N 64
463 463 522	537 540 563	447 489 810	283 303 303	311	411
29.0	0.00	28.7 28.7 28.7	28 28.4 28.4 4.4.4	28.4	28.4
7 4 4 7 4 7	7 4 4 4 7 7 7	4 4 4 6 .5 7 .6 .5	4 4 4 0 0 0	44.	46
33 33 35	6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	33.0 33.0 34.0	39 410 41	444	4. 4. 4. (2)

## ALIGNMENTS

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hypothetical protein 63B12.4 - fruit fly (Drosophila melanogaster)
C;Species Drosophila melanogaster
C;Species 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C;Accession: T12682
R;Ferraz. C; Vidai, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Ferraz. C; Vidai, S.; Brun, C.; Bucheton, A.; Demaille, J.G.
R;Reference number: Drad Library, January 1998
A;Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A;Reference number: 217572
A;Cecssion: T12682
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-289 < FER.
A;Cross-references: UNIPROT:046084; EMBL:AL021106; NID:e1371406; PID:e1249575; PIDN:CA*
A;Experimental source: clone cosmid 63B12
A;Cross-references: FlyBase:FBgn0000117
A;Introns: 186/3
A;Note: 63B12.4
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Best Local Similarity 59.4%; Pred. No. 2.4e-06;
Matches 19; Conservative 6; Mismatches 7; Indels
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RESULT 2 T16702 hypothetical protein R07G3.5 - Caenorhabditis elegans	C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T16702	Ayloumitted to the EMBL Data Library, July 1995 Aybescription: The sequence of C. elegans cosmid R07G3. AyReference number: Z18562 A.Recession: T16702	A;Cratus: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residuse: 1-269 <con A:Cross-references: UNIPROT:009422; EMBL:U23452; NID:q733564; PID:q733568; PIDN:AAC467</con 	A;Experimental source: strain Bristol N2 C;Genetics: Gane: CESP:RO7G3.5 A;Introns: 62/2; 103/1; 175/3; 220/2
RESULT 2 T16702 hypothetica	C; Species: C; Date: 20 C; Accession	A; Colliferit, M. A; Description A; Reference in A; Accession:	A;Status: 1 A;Molecule A;Residues	A; Experimen C; Genetics: A; Gene: CES A; Introns:

50.6%; Score 82; DB 2; Length 269; 56.2%; Pred. No. 0.00011; Query Match Best Local Similarity N

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Gaps

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Indels

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Length 164;

DB 2;

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Gaps

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Indels

Length 236;

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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: 63416
C;Accession: 63416
Agman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
Cory, S.; Olson, M.V.
N. Lory, S.; Olson, M.V.
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic path
A;Reference number: A82950; MUID:20437337; PMID:10984043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable dioxygenase (EC 1.14.-.-) Rieske iron-sulfur component TM1284 - Thermotoga mar
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C;Accession: G72273
                                                                                                                                                                                                                                                                                                                                                              mannopine synthesis-like protein [imported] - Agrobacterium tumefaciens plasmid pAtK84b
C;Species: Agrobacterium tumefaciens
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;cross-references: UNIPROT:0912R4; GB:AE004609; GB:AE004091; NID:g9947810; PIDN:AAG052
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Genome: plasmid pAtK84b
C;Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein PA1831 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Accession: T46943
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Ablecule type: DNA
A;Residues: 1-183 cOGE>
A;Residues: 1-183 cOGE>
A;Cross-references: UNIPROT:Q9WWA7; EMBL:AF065244; PIDN:AAD31602.1
A;Experimental source: strain K84
                           13;
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1.9;
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Pred. No. 2.5;
9; Mismatches 1:
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Pred. No. 1.9;
6; Mismatches
                                                                                                                                                       2 REQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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ilarity 37.5%; Pred. No. 1.6;
Conservative 7; Mismatches
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R,Oger, P.M.; Farrand, S.K.
submitted to the EMBL Data Library, May 1998
A,Reference number: Z24140
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Best Local Similarity 33.3%;
Matches 10; Conservative
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Best Local Similarity 43.8%;
Matches 14; Conservative
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hes 12; Conserv
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A, Status: preliminary
A, Molecule type: DNA
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A/Molecule type: DNA
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C.Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. PCC 7120
A;Note: Nostoc sp. Strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C;Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004
C;Accession: AE1834
B;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A;Reference number: AB1807; MUID:21595285; PMID:11759840
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*Residues: 1-164 «KUR»
A;Cross-references: UNIPROT:Q8Z077; GB:BA000019; PIDN:BAB77745.1; PID:g17135199; GSPDB:G
A;Experimental source: strain PCC 7120
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Keywords: phospholistidine; phosphoprotein
F:19-201/Domain: phosphoglycerate mutase homology <PGNH>
F:24/Active site: His (phosphohistidine intermediate) #status predicted
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A,Residues: 1-20 ocHW-
A,Cross-references: EMBL: 889633; NID:g1279694; PIDN:CAA61787.1; PID:g1279707
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
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                                                                                                                                                                                                                                                                                                                               hypothetical protein YOR283w - yeast (Saccharomyces cerevisiae)
NiAlternate names: hypothetical protein 05480
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Accession: S67185; S72052
R;Cheret, G; Sor, F;
R;Cheret, G; Sor, Fein Sequence Database, July 1996
A;Reference number: S67169
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A;Gene: alr0221
C;Superfamily: Escherichia coli phosphohistidine phosphatase sixA
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   Indels
   10;
                                                                                                                               Score 55; DB 2. Pred. No. 1.2; 5; Mismatches
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                                                                               2 RECAELTGLRLASLGLKFNKIVHSSMTRAIET
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Best Local Similarity 41.9%;
Matches 13; Conservative
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A,Cross-references: SGD:S0005809
A,Map position: 15R
Conservative
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       Matches
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phosphoglyceromutase I homolog lin2308 [imported] - Listeria innocua (strain Clip11262)
C; Species: Listeria innocua
C; Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 16-Aug-2004
C; Accession: All 120
R; datession: All 120
R; dateser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecke
i, Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, F.
D; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Nos, C.; Schluteter, T.; Simces, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Scatus: preliminary
A;Molecule type: DNA
A;Accession: All 120
A;Status: preliminary
A;Molecule type: DNA
A;Cross-references: UNIPROT:092908; GB:AL592022; PIDN:CAC97536.1; PID:g16414820; GSPDB: A;Cross-references: UNIPROT:0911262
C;Genetics:
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A;Accession: A83508
A;Status: prelimary
A;Molecule type: DNA
A;Residues: 1-98 <STO>
A;Accoss-references: UNIPROT:Q914N5; GB:AE004540; GB:AE004091; NID:g9947008; PIDN:AAG04.
A;Experimental source: strain PAO1
C;Genetics:
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1350
A;Accession: AB1350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-229 <GLA>
A;Residues: 1-229 <GLA>
A;Cross-references: UNIPROT:Q8Y571; GB:NC_003210; PIDN:CAD00283.1; PID:g16411675; GSPDB
A;Experimental source: strain EGD-e
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C;Superfamily: Cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homc
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C;Superfamily: Cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase
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C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: A83508
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbic, Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52; DB 2; Length 229;
Pred. No. 3.4;
6; Mismatches 12; Indels
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Best Local Similarity 40.0%;
Matches 12; Conservative 6
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RyPleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, P. Gocayre, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kirkness, E.F.; Kerlavage, P. Gocayre, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.; Bradon, R.C.; Fine, L.D.; Fritchman, J.L.; Glodek, A.; Kelley, J.M.; Weidman, J.L.; Georga, G. Gocard, M.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Reference number: A64000; MUID:95350630; PMID:7542800
A; Returns: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-27 < TIGR>
A; Residues: 1-27 < TIGR>
A; Residues: 1-27 < TIGR>
A; Cross-references: UNIPROT:P44865; GB:U32760; GB:L42023; NID:G1573764; PIDN:AAC22416.1;
C; Superfamily: Cofactor-dependent phosphoglycerate mutase; phospholistidine; phosphoprotein
F; 3-216/Domain: phosphoglycerate mutase homology < PGYM+
F; 3-216/Domain: phosphoglycerate mutase homology < PGYM+
F; 3-216/Domain: phosphoglycerate mutase homology < PGYM+
F; 3-216/Domain: phosphoglycerate mutase homology < PGYM+
F; 8/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                       Nature 399, 323-329, 1999

A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A, Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq A, Reference number: 472203

A, Reference number: 472203

A, Status: preliminary

A, Molecule type: DNA

A, Residues: 1-331 < ARN>
A, Fasperimental: Source: Strain MSB8

C, Genetics: A, Genetics: B, Ge
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Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
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32.1%; Score 52; DB 2; Length 227;
Best Local Similarity 38.7%; Pred. No. 3.4;
Matches 12; Conservative 7; Mismatches 12; Indels
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Pred. No. 4.3;
4; Mismatches 9;
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Best Local Similarity 43.8%;
Matches 14; Conservative
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M.J., E K., Lin

P.; Hickey, A.; Larbig,

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Gaps

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Gaps

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C;Keywords: intramolecular transferase; isomerase

A; Gene: PA1096

Matches

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Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, Leuss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:092D28; GB:AJ235270; GB:AJ235269; NID:G3860572; PIDN:CAA146
A;Experimental source: strain Madrid E
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R;Andersson, S.G.B.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature: 396, 133-140, 1998

A;Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A;Reference number: A71630; MUID:99039499; PMID:9823893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1368 <AND>
                                                                                                                                                                                                                                                                                                                                            hypothetical protein RP165 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Date: 02-Peb-2001 #sequence_revision 02-Peb-2001 #text_change 09-Jul-2004
C.Accession: G84564
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   Length 217;
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                                                                 Indels
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      DB 2;
Score 50; DB;
Pred. No. 6.4;
7; Mismatches
                                    6.4;
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                                                                                                                             4 QAELTGLRLASLGLKFNKIVHSSMTRA 30
                                                                                                                                                                                        47 EAKAAGORLKAAGLKFDIAYTSALSRA 73
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   Query Match
Best Local Similarity 40.7%;
Matches 11; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 11; Conserv
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A;Molecule type: DNA
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A;Residues: 1-211 <NAI>
A;Cross-references: UNIPROT:P36623; EMBL:X75385; NID:g407526; PIDN:CAA53154.1; PID:g4075
R;Brown, D.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A;Reference number: 221792
A;Accession: T38414
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AF3540
A;Accession: AF3540
A;Residuas: Dreliminary
A;Molecule type: DNA
A;Residuas: 1-217 cKUR>
A;Residuas: 1-217 cKUR>
A;Cross-references: GB:AE008918; PIDN:AAL53489.1; PID:g17984392; GSPDB:GN00191
A;Experimental source: strain 16M
                                                                                                                                                                                                                                                                                                                                  phosphoglycerate mutase (EC 5.4.2.1) - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: 31-Dec-1993 #sequence revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: 54369; T38414; 543214
R;Nairn, J.; Price, N.C.; Fothergill-Gilmore, L.A.; Walker, G.E.; Fothergill, J.E.; Dunk Biochem, J. 297, 603-608, 1994
R;Nairn, J.; Price, N.C.; Fothergill-Gilmore, L.A.; Walker, G.E.; Fothergill, J.E.; Dunk A;Reference number: 843369; MUID:94153336; PMID:8110200
A;Accession: 543369;
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C;Superfamily: cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol
C;Superfamily: cofactor-dependent phosphoglycerate mutase homolecular transferase; isomerase; phosphoh
F;10-198/Domain: phosphoglycerate mutase homology <PGMHs
F;10-198/Domain: phosphoglycerate mutase homology <PGMHs
F;14,66,163/Active site: Arg, Arg, His #status predicted
F;15/Active site: His (phosphohistidine intermediate) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: II
C;Superfamily: Cofactor-dependent phosphoglycerate mutase; phosphoglycerate mutase homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphoglycerate mutase (EC 5.4.2.1) [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 16-Aug-2004 C;Accession: AF3540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: EMBL:273100, PIDN:CAA97363.1; GSPDB:GN00066; SPDB:SPAC26F1.06
A,Experimental source: strain 972h-; cosmid c26F1
C,Genetics:
A,Gene: SPAC26F1.06
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                                                                        Gaps
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         Length 98;
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Local Similarity 41.9%; Pred. No. 4.4;
les 13; Conservative 7; Mismatches 11: Indels
                                                                        Indels
      Score 51.5; DB 2;
Pred. No. 1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: DNA
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                                                                                                                                1 CREQ----AELTGLRLASLGLK 18
                                                                                                                                                                       31.8%;
56.5%;
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Gene: BMEII0248
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November 10, 2004, 13:38:57; Search time 43.9585 Seconds (without alignments) 431.938 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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162
1 CREQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          1825181 seqs, 575374646 residues
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                                                                              OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Q9k466 streptomyce
SUMMARIES	XXOXADHOLORHORUNDINOLORYORUN XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX	Q9K466
DB	000000000000000000000000000000000000000	2
Length	4 6 7 8 8 8 8 9 4 4 4 8 8 8 8 9 1 1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	208
% Query Match		32.7
Score	823 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	53
Result No.	11111111111111111111111111111111111111	

Q9cku9 pasteurella Q74119 lactobacilla A808146 lactobaci Q8823 pseudomonas Q912r4 pseudomonas Q7rs23 plasmodium Q7xyx cryptospori Q9x10 thermotoga Q8dv49 streptococc Q88yy lactobacilla P44865 haemophilus Q929g8 listeria in Q71xg0 listeria mo Q8y571 listeria mo Q8y571 listeria mo	rs  te update)  tion update)  tion update)  Vertebrata; Euteleostomi;  I; Hominidae; Homo.  tt M., Kreider B.L.;  n of Bcl-XL-binding Proteins  lay Libraries.";	7/1 C C D S 2 1 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3
227 1 GPMA_PASMU 230 1 GPA1_LACJO 230 2 AASOB146 236 2 Q8B2A3 236 2 Q912R4 316 2 Q7RS23 317 2 Q7YXT7 331 2 Q9X110 132 2 QBDU49 225 1 GPMA_HAEIN 229 1 GPMA_LISIN	PRT; 34 AP 19, Created) 19, Last sequence 19, Last annotation 68 (Fragment). data; Craniata; Ver ates; Catarrhini; P ates; Catarrhini; P characterization of cific mRNA Display -20906(2001).	100.0%; Score 162; 100.0%; Score 162; 100.0%; Pred. No. 5. 100.0%; Pred. No. 6. 100.0%; Pred. No. 6. 100.0%; Pred. No. 6. 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100.0%; PRT; 255 100
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D., Statchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong D., Brownstein M., Soars M.B., Bonaldo M.F., Carninci P., Frange C., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffaud G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.,
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TISSUB-EMPTYO;

MEDINE-22388257; PubMed=12477932;

MEDINE-22388257; PubMed=12477932;

Atausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Antschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Carahnof D., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Brownstein M.J., Widhi T.B., Toofhlyuki S., Carahnof P., Prange C.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.J.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Makeley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Annes S.J., Marra M.A.;
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-JUN-2003 (TrEMBLrel. 26, Last annotation update)
2610528A17Rik protein (Fragment).
Name=2610528A17Rik;
Nus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
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Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC008196; AAH08196.1; -.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein.
SEQUENCE 255 AA; 28006 MW; 07B881C338BE033C CRC64;
                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                          94.4%; Score 153; DB 2; L
100.0%; Pred. No. 1.6e-14;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 REQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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                                                                                                                                                                                                                                                                                                                                                    nterPro, IPR001345; PG/BPGM_mutase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                cDNA sequences."
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                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                       IISSUE=Cervix;
                                                                                                                                                                                                                  and mouse
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Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-EMBYONIC body between diaphragm region and neck;
MEDLINE-20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 12 days embryon embryonic body between diaphragm region and neck cDNA, RIKEN full-length enriched library, clone:943001H113 product:hypothetical Phosphoglycerate mutase family containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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MEDLINE=21085660; PubMed=11217851;
RIKEN FANTOM Consortium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Embryonic body between diaphragm region and neck; The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryonic body between diaphragm region and neck; MEDILINE=99279253; PubMed=1034966; Carninci P., Hayashizaki Y.; "High-efficiency full-length cDNA cloning.";
                                                                                                                                                                      Strausberg R.;
Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                      282 AA; 31289 MW; FE0852E1DC06A414 CRC64;
                          and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93.8%; Score 152; DB 2; L
ilarity 96.9%; Pred. No. 2.6e-14;
Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118 REQAELTGLRLASLGLKFNKIVHSSMTRAVET 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 REQAELIGLRLASLGLKFNKIVHSSMTRAIET 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  287 AA.
                                                                                                                                                                                                                     EMBL; BC052179; AAH52179.1;

MGD; MGI.1919792; Z610528417Ri.

GO; GO:0003824; F:catalytic activity; IBA.

GO; GO:0008152; P:metabolism; IBA.

InterPro; IPR001345; PG/BPGM_mutase.

Pfam; PF00300; PGAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein, full insert sequence.
Name=2610528A17Rik;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Mouse)
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                                                                                                            SEQUENCE FROM N.A. TISSUE=Embryo;
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Q8BM78;
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Adachi J. Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Harabaida K., Hayatsun M., Hanagaki T., Hara A., Hashizume W. Tricotani K., Hayatsun W., Hirozana T., Arachi H., Kawai J., Kojima Y., Kohofo S., Konno H., Kouda M., Koya S., Katoh H., Kawai J., Kojima Y., Kohofo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Murata M., Murata M., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Asakai C., Sakai K., Sakauna N., Sakauna M., Ohsato N., Okazaki Y., Asakai C., Sakai K., Sakauna N., Sakai M., Atagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tagami M., Submitted (Jul.-2001) to the Embl./GenBank/DDBJ databases.

Embl. AK014588: BAC28763 1; -MBL/GenBank/DDBJ databases.

ROJ GO:0003824; F:catalytic activity; IEA.

InterPro: IPRO0130; PRO1345; PG/BPGM_mutase.

Hypothetical protein.
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.; "Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes."; Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-071-2003 (TrEMBLrel. 23, Last sequence update)
Mus musculus ES cells cDNA, RIKEN full-length enriched library,
clone:0330016f19 product:hypothetical Phosphoglycerate mutase family
Name=261055BATRik;
Mus musculus ESBATRik;
                                                                             TISSUBL/65;
TISSUBL/65;
TISSUBL/65;
TISSUBL-EARLYOOLC DODAY Detween diaphragm region and neck;
TISSUB-EMBLYOOLC DAY
MEDGINS-20530913; PubMed-11076861;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Ltoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Fujiwake S., Inoue K., Tazawa M., Ohara E., Watshiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Nokazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
"RIKEN integrated sequence analysis (RISA) system-384-format
Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
0
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287 AA; 31884 MW; E9B25B1B148F7FD6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 152; DB 2; L 96.9%; Pred. No. 2.6e-14; Live 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 REQAELTGLRLASLGLKFNKIVHSSMTRAVET 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 REQAELTGLRLASLGLKFNKIVHSSMTRAIET 33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=99279253; Pubmed=10349636;
Carninci P., Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 96.9
Matches 31, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=CS7BL/6J;
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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Q8BX10;
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The FANTON Consortium, the RIKEN Genome Exploration Research Group Phase I & II Team; the RIKEN Genome Exploration Research Group Phase I & II Team; manalysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J;
MRDLINB=20499374; PubMed=11042159;
REDLINB=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Directive 2019 (197) PubNed=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P., Kohibata K., Itoh M., Aizawa K., Kituani T., Tashiro H., Itoh M., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watshiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; Rikis integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                                                                     RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
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Pred. No. 2.6e-14;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31994 MW; B704CDF4E640F888 CRC64;
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"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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MGD; MG11919792; 2610528417Rix.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
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                                                                                                                                                                 STRAIN=C57BL/6J;
MEDLINE=21085660; PubMed=11217851;
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Best Local Similarity 96.9%;
Matches 31; Conservative
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Xenopus laevis (African clawed frog).
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                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                    LOC398484 protein (Fragment)
Name=LOC398484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dev. Dyn. 225:384-391(2002).
                                                                                                                                                                                                          30; Conservative
                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopodinae; Xenopus.
                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2003
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Q8AVL5;
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Matches
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STRAIR-CSPEL/G17 IISSUE=Whole body;
MEDLINE=CSPEL/G17 IISSUE=Whole body;
MEDLINE=20499374; PubMed=11042159;
Carninci P., Shibata Y., Hayatsu N., Sayashizan Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizani Y.,
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRANIE-STBL/G1; TISSUE=Whole body;
The FANTOM CONSORTIUM.
THE RIKEN GENOME Exploration Research Group Phase I & II Team;
The RIKEN GENOME Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
Nature 420:553-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-CSTEL/6J; TISSUE-Whole body,
Adachi J., Alzawa K., Akahira S., Akimura T., Arai A., Aono H.,
Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
Okazaki Y., Okido T., Owa C., Saito H., Saito H., Sasaki C., Sakai K.,
Sano H., Sasaki D., Shibata K., Shibata Y., Shinaqawa A., Shiraki T.,
Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=20530913; PubMed=11076861; Sasaki N., Carninci P., Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Shibata Y., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P., Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Fujiwake S., Inoue K., Togawa W., Izawa M., Ohara E., Watshiwagi K., Fujiwake S., Inoue K., Togawa W., Tanaka T., Matsuura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.; RIKEN integrated sequence analysis (RISA) system-184-format Genome Res. 10:1757-1771(2000).
                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6J; TISSUE=Whole body;
MEDLINE=21085660; PubMed=11217851;
RIKEN FANYOM CONSORTIUM;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690(2001).
                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OT-2003 (TrEMBLrel. 25, Last annotation update)
Mus musculus 10 days embryo whole body cDNA, RIKEN full-length
enriched library, clone:2610528A17 product:hypothetical
Phosphoglycerate mutase family containing protein, full insert
                                                                                                                                                                                                                                                                STRAIN=CS7BL/60; TISSUE=Whole body;
MEDLINE=99279253; PubMed=10349636;
Carninci P., Hayashizaki Y.
High-efficiency full-length ;
Meth. Enzymol. 303:19-44(1999).
                              252 AA
                              PRT;
                              PRELIMINARY;
                                                                                                                                                                               (Mouse)
                                                                                                                                                                Name=2610528A17Rik;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                Mus musculus
                                                                                                                                                  sequence
                              Q9CZU2
RESULT 6
               O9CZU2
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Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M., Muramatsu M., Hayashizaki Y.;
Submitred (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK012159; BABS067.1;
MGD; MGI:1919792; 2610528A17Rik.
MGD; MGI:1919792; Picetallytic activity; IEA.
GO; GO:0008152; Picetallytic activity; IEA.
InterPro; IPR001345; PG/BFGM_mutase.
PFGm; PF00309; PGAM; 1.
Hypochatical protein.
SEQUENCE 252 AA; 28695 MW; CC659D74D175ACD7 CRC64;
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Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetic and genomic tools for Xenopus research: The NIH Xenopus
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TISSUB-Embryo;
Klein S. Strausberg R.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.2%; Score 151; DB 2; L 93.8%; Pred. No. 3.2e-14; ive 2; Mismatches 0;
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EMBL; BC041756; AAH41756.1; -.

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01-JUN-1998
                          RESULT 9
046084
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NEUTINE=2388257; PubMed=12477932;

NEUTINE=2388257; PubMed=12477932;

NITAUSHER R.D., Feingold E.A., Grouse L.H., Derge J.G.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Rausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altschul S.F., Zeberg B. B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Rapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Rapa S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Raba S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Touchman J.W., Green B.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schutz P., Dickson M.C., Balakesley R.W., Dickson M.C.,

Ranson M. J., Schalks W., Smallus D.E., Schnerch A., Schein J.E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                           Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia; Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
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                                                                                                                                                                                                                                             Length 268;
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                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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InterPro; IPR001345; PG/BPCM_mutase.
PFfam; PF00300; PGAM; 1.
Hypothetical protein.
SEQUENCE 278 AA, 31210 MW; 67923E297F554639 CRC64;
                                                                                                                                                                            268 AA; 30564 MW; 9B0D46568A19742C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-JUL-2004 (TrEMBLrel. 27, Created)
5-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypothetical protein.
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Pred. No. 2.7e-08;
5; Mismatches 4;
                                                                                                                                                                                                                                          Score 112; DB 2;
Pred. No. 2.6e-08;
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                                                                                                                                                                                                                                                                                                     4; Mismatches
                      GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001345; PG/BPGM_mutase.
Pfam; PF00300; PGAM; I.
                                                                                                                                                                                                                                          69.18;
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1 Similarity 71.9%;
23; Conservative
                                                                                                                                                                                                   PRELIMINARY;
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Matches 23; Conserv
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                                                                                                                                                                      SEQUENCE
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Pfam; r.
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REAUGENCE FROM N.A.

REAULINE-20196006; Pubbled=10731132;

RADAGENE KORN N.A.

Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RADAGENE R.A., Lewis S.E., R.H. Holt R.A., Evans C.A., Gocayne J.D.,

RADAGENE R.A., Lewis S.E., R. Holt R.A., Evans C.A., Gocayne J.D.,

Button G.G., Mortman J.R., Yandell M.D., Zhang O., Chen L.X.,

RADAGEN R.C., Regers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RADAGEN R.C., Papayani A., An H.J., Andrews-Plannkoch C., Baldwin D.,

RADAGEN R.M., Benos P.V., Berman B.P., Bhandari D., Bolahakov S.,

Berkova D. Botchan M.R., Butler H., Cadieu E., Center A., Chandra I.,

RADAGOR K., Dougle C., Downes M., Dugan-Rocha S., Punkov B.C., Dunn P.,

Buttis R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RADAGOR K., Douglis R., Downes M., Dugan-Rocha S., Pleischmann W.,

RADAGOR K., Doug L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RADAGOR K., Doug L.E., Downes M., Dugan-Rocha S., Pleischmann W.,

RADAGOR K., Doug L.E., Lownes M. S., Gelbart W.M., Glasser K.,

RADAGOR K., Doug L.E., Mowland T.J., Hernandez J.R., Houck J.,

Alali M., Harvey D., Heaman T.J., Hernandez J.R., Houck J.,

Alali M., Multh P., Karpen G.H., Ke Z., Kennison J., Li Z.,

Lida Y., Lank R., Moy M., Murphy B., Mocheod M.P., McDherson D.,

And Merkulov G., Milshina N.V., Mobarry C., Morris G., Woshrefi A.,

Radazolo M., Pittenan G., Pan S., Pollard J., Puri V., Reese M.G.,

RADAGOR S., Pachington K., Saunders R.D., Scheler F., Shen H.,

Radazolo M., Pittenan G., Pan S., Pollard J., Puri V., Resee M.G.,

Rader R., Remington K., Strong K., Wu D., Strong R., Smith T.,

Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Smith T.,

Radazolo M., Wassarman D.A., Weiter E., Wang A., Waller E., Wang K., Smith R.,

Mulliams S.M., Woodager, Wolley K., Chu D., Yang S., Yao Q., Yao Z.,

Rance R. M., Woyers B.W., Rubin G.W., Venter E., Wang S., Yao Q., Yao Z.,

Rance R. M., Wyers B.W., Rubin G.W., Venter J.C.;

Rance R. M., Woyers B.W., Rubin G.W., Venter E.,

Rance R. M., Woyers B.W., Rubin G.W., Vent
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MEDLINE=22426655; PubMed=12537568;

Celniker S.B., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Ascled J.M., Park S., Pfeiffer B.D., Richards S., Sodergen E.J., Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M., Finishing a whole-genome shorgun: release 3 of the Drosophila melanogaster euchromatic genome sequence.", Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                             Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                   Last sequence update)
Last annotation update)
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Kaminker J.S., Bergman C.M., Kronmiller B., Ca
Patel S., Frise E., Wheeler D.A., Lewis S.E.,
  289
                                             Created)
PRT;
                                                                                      05-JUL-2004 (TrEMBLrel. 27, Last an CG14816-PA (EG:63B12.4 protein).
Name=EG:63B12.4; ORFNames=CG14816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 287:2185-2195(2000).
  PRELIMINARY;
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Query Match
Best Local Similarity
Matches 19; Conserv
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Best Local Similarity
Matches 19; Conserv
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SEQUENCE FROM N.A.
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STRAIN=Bristol N2;
Connell M.;
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YROS_CAEEL
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  Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.":
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                  MEDINE=22426069; PubMed=12537572; Matthews B.B., Campbell K.S., Misser S., Crosby M.A., Mungall C.J., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P., Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Kusso S., Schroeder A.J., Shu S.Q., Strapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
                                                                                                                                                                                                                                                                                                Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota, Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 57.4%; Score 93; DB 2; Length 289; Best Local Similarity 59.4%; Pred. No. 2.1e-05; Matches 19; Conservative 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brun C., Bucheton A., Demaille J.G.; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Benos P.;
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AE0031422; AAF45678.1; -.
EMBL; ALO21106, CAA15939.1; -.
PIR; T12683; T12682.
IntAct; O46084; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33165 MW; 6DE63EE448170361 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
                                              a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase, FBgn0023517; CG14816.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
HorerPo; IPR001345; PG/BPGM_mutase.
Pfam; PF00300; PGAM; 13165 MW; 6DE63E84481
SEQUENCE 289 AA; 33165 MW; 6DE63E84481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
GH02880p (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (SEP-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
Ferraz C., Vidal S.,
Submitted (JAN-1998)
                                                                                                                                                                                                                                                                                                                                         systematic review.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FLYBASE;
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Gaps
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Eukaryota, Merazoa; Nematoda, Chromadorea; Rhabditida, Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                    Gaps
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Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.;
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Bukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota, Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 294;
                                                                                                                                                                                                                                                                                         Length 294;
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59.4%; Pred. No. 2.1e-05;
tive 6; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                             Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AV66608, AAL28156.2; -.
InterPro; IPR001345; PG/BPGM_mutase.
Pfam; PP00300; PGAM; 1.
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SEQUENCE 294 AA; 33625 MW; 57323DC668120198 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
GH02080 (Fragment).
EG:63B12.4.
                                                                                                                                                                                                                                                                                         57.4%; Score 93; DB 2; Lei
ilarity 59.4%; Pred. No. 2.1e-05;
Conservative 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-007-1997 (Rel. 35, Created)
10-00T-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Hypothetical protein R07G3.5 in chromosome II
ORFNames=R07G3.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 RKÇABFTGKRLCELGIKWDKVVASTMVRAQET 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 AA.
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RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
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RAMEDLINE-20196006; PubMed=10731132;
RAMEDLINE-20196006; PubMed=10731132;
RAMEDLIONE-20196006; PubMed=10731132;
RAMEDLIONE-20196006; PubMed=10731132;
RAMEDLIONE-20196006; PubMed=10731132;
RAMEDLIONE-20196006; PubMed=10731132;
RAMEDRAM M. Band M. Barddell M.D. Sandmech C., Baldwin D., RAMEDRAW S., Baldwar M.R., Bandwar D., Bordmarch C., Bardwech P., Bortner P. Brotteier P., Bortwar D., Bordman M., Bouck J., Bordstein P., Brotteier P., Bortwar D., Boldhardwar S., Dulmkov B.C., Dunn P., Ramel B., Delcher A., Domg Z., Mays A.D., Daw I., Dietz S.M., Durbin K.J., Doup L.E., Downes M. Dugan-Rocha S., Plaischmann W., Roben R., Borden R., Bordelista C.C., Ferraz C., Ferriars S., Flasschmann W., Albarin D., Harris M.J., Harvey D., Helmann T.J., Herrandez J.R., Houck J., Landy Y., Lin X., Aldali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethok M., Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Mattei B., McIntodh T.C., Morsker D., Put V., Mattei B., McIntodh T.C., Musskern D.R., Packeb J.M., Ralman G.S., Pan S., Pollard J., Put V., Reese M.G., Ramer S., Pollard J., Wardy S., Sinch T., Sanden S., Pand S., Ston H., Wallen R., Senden S., Pand S., Pollard J., Wang X., Wallen R.K., Remington K., Stong R., Stong R., Stong R., Stong R., Stong R., Stong S., Yao Q.A., Yang X., Wallen R., Wallen R., Wolley W., Zhong R., Stong S., Yao Q.A., Yang X., Wallen R., Wallen G., Standers R.D., Stong D., Wang X., Wallen R., Wallen G., Standers R.D., Stong C., Zhan M., Zhong W., Zhong W., Zhong W., Zhong Y., Stong C., Zhan M., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong Y., Wallen R.M., WoodageT, Worley R.W., Wolley W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong W., Zhong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22426065; PubMed=12537568;
Celniker S.E., Meeler D.A., Krommiller B., Carlson J.W., Halpern A., Celniker S.E., Meeler D.A., Krommiller B., Erise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren B.J., Svirskas R., Stapheron E.J., Mers E.W., Gibbs R.A., Rubin G.G., Venter C., Weinscock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; Finishing a Wold-eqenome shotgun: release 3 of the Drosophila melanogaster euchromatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                            Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa; Arthropoda; Hakapoda; Insecta; Pterygota;
Neoptera; Endobterygota; Diptera; Brachycera; Muscomorpha;
Brhydroidea; Drosophilidae; Drosophila.
     Last sequence update)
Last annotation update)
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Senome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
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     01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
                                                                          ORFNames=CG15874;
       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Nematocera, Culicoidea, Anopheles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Anopheles Genome Sequencing Consortium,
Submitted (ARR-2003) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10; Indels
                                                                     Waterston R.;
Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      284 AA; 32490 MW; 820D56CE79E71F90 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32423 MW; C9B01EF80B5859F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
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Pred. No. 0.00094;
4; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               119 REQAELLGKRLANSDIKFTNMTMSTMVRATET 150
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EMBL; AAABO1008859; EAA07503.2; -.
GO; GO:0003824; F:catalytric activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IPR001345; PG/BPGM_mutase.
Pfam; PF00300; PGAM; I.
                                                                                                                                                                                                                                                                                                                                                                                  WormPep; R0763.5; CB31979.
InterPro; IPR001345; PG/BPGM_mutase.
Pfam; PF00300; PGAM; 1.
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                                                                                                                                                                                                                                                                                                                                      EMBL; U23452; AAK31545.2; -.
PIR; T16702; T16702.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 50.6%;
Local Similarity 56.2%;
les 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2004 (TrEMBLrel. 26, 01-MAR-2004 (TrEMBLrel. 26, 101-MAR-2004 (TrEMBLrel. 26, 101-MAR-2004) (TrEMBLrel. 26, 101-MANGPO0000021127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                285 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=180454;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical
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                         [2]
REVISIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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ID Q9W173
AC Q9W173;
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RESULT 13

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Best Loca Matches

RESULT 14

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TISSUB-Embryo,

WEDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

Ratasberg R.L., Collins F.S., Wargner L., Shenmen C.M., Schuler G.D.,

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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,

Norden M., Saares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabb S.R.,

Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gabbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Boulfard G.G.,

Ratesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schein J.E.,

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Rodriguez A.D., Marra M.A.,

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Rodriguez A.D., Marra M.A.,

Rodriguez A.D., Schmutz J., Myers R.M., Scheit J.E.,

Rodriguez A.D., Marra M.A.,

Rodriguez A.D., Schmutz J.,

Rodriguez A.D., Schmutz J.,

Rodriguez
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                 Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfied B.J., Bayrakearoglu L., Berman B.P. Bettencourt B.R., Celniker S.E., Gergy A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                  "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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53.1%; Pred. No. 0.0053;
iive 5; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases. EMBL; AE003464; AAF47204.1; -... FlyBase; Regn0035004; G18894.
GO; GO:0003824; F:catalytic activity; IEA.
GO; GO:0008152; P:metabolism; IEA.
InterPro; IRR001345; PG(BPGM mutase.
PF00300; PGAM; 1... SAEAF130DF1AAC59 CRC64; SEQUENCE 280 AA; 31395 MW; SAEAF130DF1AAC59 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-UUL-2004 (TrEMBLrel. 27, Created)
05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-UUL-2004 (TrEMBLrel. 27, Last annotation update)
Hypotheital protein.
Xenopus laevis (African clawed frog)
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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                      systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002)
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MEDLINE=22426069; PubMed=12537572;
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Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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NCBI_TaxID=8355;
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                                                                                                                                                                                              Lewis S.E.;
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                                              Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W., Richardson P., "Genetic and genomic tools for Xenopus research: The NIH Xenopus
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                                                                                                                                                                                                                                                                                                                   Length 259;
                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                              Klein S., Strausberg R.; Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases. EMBL; BC073429; AAH73429.1; "InterPro; IPR001345; PG/BFGM_mutase. InterPro; IPR005952; Phosphogly_mut1. Pf00300; PGAM; 1.
                                                                                                                                                                                                                                           TIGREAMS, TIGNO1258; pgm_1; 1.
TIGREAMS, TIGNO1258; pgm_1; 1.
HYPOTHETICAL protein.
SEQUENCE 259 AA; 29622 MW; FECO0BD6627EAF96 CRC64;
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د.
                                                                                                                                                                                                                                                                                                                 36.4%; Score 59; DB 2; 38.7%; Pred. No. 2.5; iive 10; Mismatches
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MEDLINE=22341132; PubMed=12454917;
MEDLINE=22341132; PubMed=12454917;
                                                                                            initiative.";
Dev. Dyn. 225:384-391(2002)
                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 12; Conservative
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          FROM N.A.
                                                                                                                                    SEQUENCE
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Search completed: November 10, 2004, 14:50:16 Job time : 45.9585 secs

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Sequence 141, Application US/10012542
Patent No. 6627741
GENERAL INDERMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 94 Human Secreted Proteins
TITLE REFERENCE: PZ02991
CURRENT APPLICATION NUMBER: US/10/012,542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
CRGANISM: Homo sapiens
US-09-461-325-141
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US-10-012-542-141
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Sequence 141, App
Sequence 13251, Ap
Sequence 13251, Ap
Sequence 23, Appl
Sequence 23, Appli
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Sequence 3559, Ap
Sequence 22998, A
Sequence 9, Appli
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Appli
                                                                                                               November 10, 2004, 13:44:14; Search time 8.05283 Seconds (without alignments) 181.178 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                             478139
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.: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
.: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
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  5.1.6
Compugen Ltd.
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US-10-11-112-141
US-10-11-112-13-141
US-09-489-039A-13251
US-08-836-134-23
US-08-949-734-23
US-09-949-784-2
US-09-949-784-2
US-09-493-784-2
US-09-493-784-2
US-09-270-76-39447
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US-09-36-35-991A-22998
US-09-36-35-991A-22998
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GenCore version (c) 1993 - 2004
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Maximum Match 100%
Listing first 45 summaries
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1 GTRISDMLKLIADTWQRNCCPA 22
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Gapop 10.0 , Gapext
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Match Length DB
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Maximum DB
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1, Appli
26807, A
8, Appli
1985, Ap
1985, Ap
1985, Ap
1983, Ap
3, Appli
5, Appli
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8, Appli
15, Appl
23152, A
6478, Ap
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Sequence 2, 2 Sequence 15, 2 Sequence 231; Sequence 232; Sequence 332 Sequence 1, 2 Sequence 3, 4 Sequence 1, 3 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Sequence 3, 4 Se
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US-09-847-524-2

US-09-438-046-15

US-09-438-046-15

US-09-252-991A-23152

US-09-543-681A-6478

US-09-270-76-53270

US-09-270-76-53270

US-09-469-185-1

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US-09-469-185-1

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US-09-281-795-3

US-09-281-786-3

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US-09-291-786-3

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US-09-291-786-3
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TITLE OF INVENTION: 94 Human Secreted Proteins
TITLE REFERENCE: P2029H
CURRENT APPLICATION NUMBER: US/09/461,325A
CURRENT FILING DATE: 1999-12-14
EARLIER FILING DATE: 1999-06-15
EARLIER FILING DATE: 1999-06-15
EARLIER APPLICATION NUMBER: 60/089,507
EARLIER APPLICATION NUMBER: 60/089,508
EARLIER APPLICATION NUMBER: 60/089,509
EARLIER FILING DATE: 1998-06-16
EARLIER FILING DATE: 1998-06-16
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EARLIER APPLICATION NUMBER: 60/090,113
EARLIER FILING DATE: 1998-06-22
NUMBER OF SEQ ID NOS: 532
NUMBER OF SEQ ID NOS: 532
EARLIER FILING DATE: 1998-06-22
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NUMBER OF SEQ ID NOS: 532
EARLIER FILING DATE: 1098-06-22
EARLIER FILING DATE: 1098-06-22
NUMBER OF SEQ ID NOS: 532
EARLIER FILING DATE: 1098-06-22
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47.6%; Pred. No. 3.3;
tive 4; Mismatches
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US-09-461-325-141
Sequence 141, Application US/09461325A
; Patent No. 6475753
, GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 47.6
Matches 10; Conservative
     358
358
1213
1213
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1009
1109
1109
1109
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212
2212
243
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     2266666666666444444
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Query Match
Best Local Similarity
Matches 8; Conserva
               IS-09-489-039A-13251
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 09/461,325
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
PRIOR APPLICATION NUMBER: BARLIER PELICATION NUMBER: 60/089,507
PRIOR FILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR PLING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/089,509
PRIOR PILING DATE: BARLIER FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/090,112
PRIOR PELING DATE: BARLIER PILING DATE: 1998-06-22
PRIOR FILING DATE: BARLIER PILING DATE: 1998-06-22
PRIOR FILING DATE: BARLIER PILING DATE: 1998-06-22
PRIOR PILING DATE: BARLIER PILING DATE: 1998-06-22
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41.5%; Score 51; DB 4; Length 325;
Best Local Similarity 47.6%; Pred. No. 3.3;
Matches 10; Conservative 4; Mismatches 3; Indels
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Patent No. 6774216
GENERAL INFORMATION:
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Matches 10; Conservative
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US-10-012-542-141
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ORGANISM: Homo sapiens
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13251
LENGTH: 498
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GENERAL INFORMATION:

APPLICANT: Mackenzie, Alex E.

APPLICANT: Mackenzie, Mani S.

APPLICANT: Mahadevan, Mani S.

APPLICANT: Mchael

APPLICANT: Mchael

APPLICANT: Mchael

APPLICANT: No. 6020127

TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy

FILE REFERENCE: 3477-112, 033477/139914

CURRENT APPLICATION NUMBER: US/08/836,134A

CURRENT FILING DATE: 1997-06-20

NUMBER OF SEQ ID NOS: 23

SOFTWARE: Patentin Ver. 2.0

SEQ ID NOS: 23
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11arity 53.3%; Pred. No. 56;
Conservative 1; Mismatches 6; Indels
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Pred. No. 7.6;
4; Mismatches 3; Indels
Sequence 13251, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
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; Patent No. 6020127
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Patent No. 6429011
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CRGANISM: Klebsiella pneumoniae
US-09-489-039A-13251
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Best Local Similarity 52.6%;
Matches 10; Conservative
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McLean, Michael
Roy, Natalie
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APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert
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US-08-836-134-23
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Sequence 3, Application US/09705872
Patent No. 6617429
GENERAL INFORMATION:
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Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                  Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                    TYPE: PRT
, ORGANISM: Homo sapiens
US-09-493-784-2
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SOFTWARE: Patentin Ve
SEQ ID NO 3
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US-09-705-872-1
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APPLICANT Mackenzie, Alex E.
APPLICANT: Mackenzie, Alex E.
APPLICANT: Mackenzie, Robert G.
APPLICANT: Mackenzie, Michael
APPLICANT: McLean, Michael
APPLICANT: McLean, Michael
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Roy, Natalie
APPLICANT: Neda, Joh-
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFERENCE: 3477-112, 033477/119914
CURRENT APPLICATION NUMBER: 1990-66-20
NUMBER OF SEQ ID NOS: 23
APPLICANT: Ikeda, Joh-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6429011
TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy
FILE REFRENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/09/493, 784
CURRENT FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 08/836, 134
PRIOR PLING DATE: 1997-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
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APPLICANT: Ikeda, Joh-e
TITLE OF INVENTION: Neuronal Apoptosis Inhibitor Protein, Gene Sequence and
Patent No. 6429011
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Pred. No. 56;
1; Mismatches 6; Indels
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Pred. No. 60;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 2, Application US/08836134A; Patent No. 6020127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09493784
Patent No. 6429011
GENERAL INFORMATION:
APPLICANT: Mackenzie, Alex E.
APPLICANT: Korneluk, Robert G.
                                                                                                                                                                                                                                                                                                                                       38.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                488 LLKKIAFLWASGCCP 502
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Best Local Similarity 53.3%;
Matches 8; Conservative
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McLean, Michael
Roy, Natalie
                                                                                                                                                                                                                                                                                                                                                                                                                       7 MLKLIADTWQRNCCP 21
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Best Local Similarity 53.3*
....has 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                             , ORGANISM: Homo sapiens
US-09-493-784-23
                                                                                                                                                                                                                       SEQ ID NO 23
LENGTH: 1151
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US-09-493-784-2
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US-08-836-134-2
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APPLICANT:
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Sequence 1, Application US/09705872
; Sequence 1, Application US/09705872
; Patent No. 6617439
; GENERAL INFORMATION:
; APPLICANT: Uoh-2 IKEDA
; APPLICANT: Kenji XAMAMOTO
; TITLE OF INVENTION: AND CDNA THEREOF
; FILE REFERENCE: 2000-1110/LC/0553
; CURRENT APPLICATION NUMBER: US/09/705,872
; CURRENT FILING DATE: 2000-11-06
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: JOh-E IKEDA
APPLICANT: Kenji YAMAMOTO
TITLE OF INVENTION: APOPTOSIS INHIBITORY PROTEIN, GENE ENCODING THE PROTEIN
TITLE OF INVENTION: AND CDNA THEREOF
FILE REFERENCE: 2000-1110/LC/00653
CURRENT APPLICATION NUMBER: US/09/705,872
CURRENT APPLICATION NUMBER: US/09/705,872
PRIOR APPLICATION NUMBER: 09/239,797
PRIOR FILING DATE: 1999-01-29
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TITLE OF INVENTION: Mutations Causative of Spinal Muscular Atrophy FILE REPERENCE: 3477-112, 033477/139914
CURRENT APPLICATION NUMBER: US/09/493,784
CURRENT FILING DATE: 2000-01-28
PRIOR PILING DATE: 1097-06-20
RIGHT APPLICATION NUMBER: 08/836,134
PRIOR FILING DATE: 1197-06-20
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.0
LENGTH: 1232
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Pred. No. 63;
1; Mismatches 6; Indels
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RESULT 15
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GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 39447

LENGTH: 269
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APPLICANT Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT PELLING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 54664
LENGTH: 269
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                                                      Query Match
38.2%; Score 47; DB 4; Length 1403;
Best Local Similarity 53.3%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 6; Indels
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ilarity 50.0%; Pred. No. 24;
Conservative 3; Mismatches 6; Indels
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Pred. No. 24;
3; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Xaa means any amino acid
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US-09-252-991A-21557
; Sequence 21557, Application US/09252991A
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US-09-270-767-39447
; Sequence 39447
; Sequence 39447, Application US/09270767
; Patent No. 6703491
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Patent No. 6703491
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                                                                                                                                           7 MLKLIADTWQRNCCP 21
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Best Local Similarity 50.0%
...hes 9; Conservative
; ORGANISM: Homo sapiens
US-09-705-872-1
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Best Local Similarity
Matches 9; Conserv
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APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANT: Keith Weinstock et al APPLICANTON: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10796-122
CURRENT FILING DATE: 1999-02-12
PRIOR PELING DATE: 1999-02-13
PRIOR PILING DATE: 1999-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 21362
GENERAL INFORMATION:
APPLICANT: MAIC O' RUbenfield et al.
APPLICANT: MAIC O' RUBenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PLING DATE: 1998-07-27
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
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Patent No. 5851817

GENERAL INFORMATION:
APPLICANT: Garbers, David L.
TITLE OF INVENTION: Species-Specific Egg-Binding Proteins of TITLE OF INVENTION: Sperm
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433
CITY: Houston
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Pred. No. 19;
2, Mismatches 2; Indels
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Pred. No. 30;
5; Mismatches
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Best Local Similarity 50.0%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.8%;
ilarity 60.0%;
Conservative
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ORGANISM: Candida albicans
US-09-248-796A-21362
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Best Local Similarity
Matches 6; Conserv
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STATE: Texas
COUNTRY: USA
COUNTRY: USA
COMPUTER READALE PORM:
MEDIUM TYRE: Flappy disk
COMPUTER READALE PORM:
MEDIUM TYRE: Flappy disk
COMPUTER: ISH PC comparible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
DAPLICATION UNMERR: US/08/276,567
CLASSIFICATION: DAME: US/08/276,567
CLASSIFICATION: US 30
ATTORNEY/AGNT INPORMATION:
MAME: Kitchell, Barbara S.
REGISTRATION NUMBER: USD.418\KIT
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
TELECOMUNICATION SEQ ID NO: 2:
SEQUENCE HARACTERISTICS:
LENGTH: 2476 amino acids
TYPE: amino acid
STRANDEDESS: single
TOPOLOGY: linear
TOPOLOGY: linear
SOLOS-276-967-2
CUBS-276-967-2
CUBS-276-967-2
CUBS-276-967-2
CUBS-276-967-2
MATCHES SMILBATLY S4.5%; Pred: No: 3.8e+02;
Matches 6; CONSERVATIVE 3; Mismatches 2; Indels 0; Gaps
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Search completed: November 10, 2004, 14:55:39 Job time: 8.10283 secs

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1. (agn2_6/ptodata1/1/pubpaa/USO7_PUBCOMB.ppp.*)

2. (agn2_6/ptodata1/1/pubpaa/USO6_PUBCOMB.ppp.*)

3. (cgn2_6/ptodata1/1/pubpaa/USO6_PUBCOMB.ppp.*)

3. (cgn2_6/ptodata1/1/pubpaa/USO6_PUBCOMB.ppp.*)

3. (cgn2_6/ptodata1/1/pubpaa/DEO7_NEW_PUB.ppp.*)

3. (cgn2_6/ptodata1/1/pubpaa/DEO8_PUBCOMB.ppp.*)

3. (cgn2_6/ptodata1/1/pubpaa/USO8_PUBCOMB.ppp.*)

4. (cgn2_6/ptodata1/1/pubpaa/USO8_PUBCOMB.ppp.*)

4. (cgn2_6/ptodata1/1/pubpaa/USO8_PUBCOMB.ppp.*)

5. (cgn2_6/ptodata1/1/pubpaa/USO8_PUBCOMB.ppp.*)

6. (cgn2_6/ptodata1/1/pubpaa/USO9_PUBCOMB.ppp.*)

7. (cgn2_6/ptodata1/1/pubpaa/USO9_PUBCOMB.ppp.*)

8. (cgn2_6/ptodata1/1/pubpaa/USO9_PUBCOMB.ppp.*)

9. (cgn2_6/ptodata1/1/pubpaa/USO10_PUBCOMB.ppp.*)

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Copyright (c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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123
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 54, Appl	Sequence 39339, A	Seguence 141, App	Seguence 141, App	Sequence 11, Appl	Sequence 2, Appli	Sequence 904, App	Seguence 204, App	Sequence 766, App	Seguence 68020, A	Sequence 218174,	Sequence 1295, Ap	Sequence 4, Appli
, OI	US-10-092-750-54	US-09-864-761-39339	US-10-012-542-141	US-10-115-123-141	4 US-10-257-022-11	US-09-835-270-2	US-10-408-765A-904	US-10-755-889-204	US-10-369-493-766	US-10-425-114-68020	US-10-424-599-218174	US-09-925-301-1295	US-10-080-943-4
DB	14	σ	14	14	14	σ	16	16	14	15	15	0	14
% Query Match Length DB ID	22	97	325	325	525	581	581	581	490	332	338	677	1698
% Query Match	100.0	41.5	41.5	41.5	41.5	41.5	41.5	41.5	40.7	40.2	40.2	39.0	39.0
Score	123	51	51	21	51	51	51	51	20	49.5	49.5	48	48
Result No.	1	α	m	4	ß	φ	7	αο	σı	10	11	12	13

RESULT 2
US-09-864-761-39339
Sequence 39339, Application US/09864761
Parent No. US20020048763A1
GENERAL INFORMATION:

47 38.2 61 15 US-10-424-599-215390 Sequence 47 38.2 203 14 US-10-059-386-33933 Sequence 47 38.2 203 14 US-10-059-386-33933 Sequence 47 38.2 729 17 US-10-055-475-12 Sequence 47 38.2 729 17 US-10-478-516-18 Sequence 47 38.2 1403 8 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-322-24 Sequence 5 US-08-913-32-24 Sequence 5 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-08-913-3 US-0		1092-750-54 ence 54, Application US/10092750 leation No. US20030032157A1 RAI INFORMATION: LICANT: Hammond, Philip W. LICANT: Hammond, Philip W. LICANT: Wright, Martin C. LICANT: Wright, Martin C. LE OF INVENTION: Polypeptides Interactive with BCL-X1 E. REPERENCE: 50036/05002 RENT FILING DATE: 20036/05002 RENT FILING DATE: 2002-03-07 OR APPLICATION NUMBER: US/10/092,750 OR FILING DATE: 2001-03-08 BER OF SEQ ID NOS: 253 TWARE: FastSEQ for Windows Version 4.0 ID NO 54 GANISM: Homo sapiens 922-750-54	<pre>Query Match</pre>
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Gaps
                                                                                                     Sequence 141. Application US/10012542

Publication No. US2030044881A1

GENERAL INFORMATION:

APPLICANTON:

APPLICANTON:

FILE REPERBNCE: P202991

CURRENT APPLICATION NUMBER: US/10/1012,542

FILE REPERBNCE: EAGLIER APPLICATION NUMBER: 08/461,325

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/461,325

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 60/089,507

PRIOR PILING DATE: EARLIER FILING DATE: 1999-12-14

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PILING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-16

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-22

PRIOR PLING DATE: EARLIER FILING DATE: 1998-06-22

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41.5%; Score 51; DB 14; Length 325;
Best Local Similarity 47.6%; Pred. No. 19;
Matches 10; Conservative 4; Mismatches 3; Indels
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITIE OF INVENTION: 94 Human Secreted Proteins
FILE OF TUNEMATION: 94 Human Secreted FILE
CURRENT APPLICATION NUMBER: US/10/115,123
CURRENT APPLICATION NUMBER: PCT/US99/13418
PRIOR PILING DATE: 1999-06-15
PRIOR FILING DATE: 1999-06-15
PRIOR FILING DATE: 1998-06-16
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Publication No. US20030065151A1
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|GSQVSSMLKLAL----QNCCP 18
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ORGANISM: Homo sapiens
US-10-012-542-141
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                                                                                                                ## APPLICANY: Hansel, David K.

### APPLICANY: Chen, Wencheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE
TOTHER TELING DATE: 2000-05-23

#### PRICE APPLICATION NUMBER: US 60/20/456

### PRICE PRICE ADDI-01-00

### PRICE PRICE ADDI-01-00

### PRICE PRICE ADDI-01-00

### PRICE PRICE ADDI-01-00

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### PRICE P
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OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN FALL LIVER, SIGNAL = 1.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
OTHER INFORMATION: EST_HUMAN HIT: W53019.1, EVALUE 7.00e-27
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41.5%; Score 51; DB 9; Length 97;
Best Local Similarity 47.6%; Pred. No. 5.5;
Matches 10; Conservative 4; Mismatches 3; Indels
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SEQ DOTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39339
LENGIH: 97
Penn, Sharron G.
Rank, David R.
Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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TYPE: PRT
ORGANISM: Homo sapiens
US-10-115-123-141

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APPLICANT: Zhang, Bing
APPLICANT: Tang, Bing
APPLICANT: Giben, Bradford W.
APPLICANT: Giben, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
APPLICANT: Glenn, Gary M.
TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REFERENCE: 660088.465
CURRENT APPLICATION NUMBER: US/10/408,765A
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SEQ ID NO 904
***TWARM: Eat
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47.6%; Pred. No. 35;
tive 4; Mismatches 3; Indels
                                                                                                                                        Sequence 2, Application US/09835270
Fatent No. US20020077462A1
GENERAL INFORMATION:
FAPLICANT: Cuttis, Rory A.
TITLE OF INVENTION: 33556, A NOVEL HUMAN TRANSPORTER AND TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 38155300080
CURRENT APPLICATION NUMBER: US/09/835,270
CURRENT FILING DATE: 2001-04-13
FRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 41.5%; Score 51; DB 9; Length 581; Best Local Similarity 47.6%; Pred. No. 35; Matches 10; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bristol-Myers Squibb Company
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 904, Application US/10408765A Publication No. US20040101874A1 GENERAL INFORMATION: APPLICANT: Ghosh, Soumitra S. APPLICANT: Pahy, Boin D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Sequence 204, Application US/10755889; Publication No. US20040171823A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258 GSQVSSMLKLAL----QNCCP 274
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258 GSQVSSMLKLAL----QNCCP 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GTRISDMLKLIADIWQRNCCP 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTRISDMLKLIADTWQRNCCP 21
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Best Local Similarity 47.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-765A-904
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
US-09-835-270-2
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US-10-755-889-204
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LENGTH: 581
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41.5%; Score 51; DB 14; Length 525;
Best Local Similarity 47.6%; Pred. No. 31;
Matches 10; Conservative 4; Mismatches 3; Indels
                             Query Match 41.5%; Score 51; DB 14; Length 325; Best Local Similarity 47.6%; Pred. No. 19; Matches 10; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LICANT: SELL.
LICANT: BALL.
LICANT: LAL, Preeti
PLICANT: LAL, Preeti
PLICANT: KERNEN, Liam
'PLICANT: KERNEN, Liam
'PLICANT: LU, Dyung Aina M.
'PLICANT: LU, Dyung Aina M.
'PLICANT: LU, Dyung Aina M.
'PPLICANT: LU, Dyung Aina M.
'PPLICANT: LU, Dyung Aina M.
'APPLICANT: LU, Dyung Aina M.
'APPLICANT: RAUMANN, Brigitte E.
'APPLICANT: Arvia. Chandra S.
'ATTLE REFERENCE: PI-0067 USN
CURRENT APPLICANTION NUMBER: US/10/257,022
CURRENT FILING DATE: 2002-10-04
'PRIOR APPLICATION NUMBER: 60/195,595
PRIOR FILING DATE: 2000-04-06
'PRIOR PELING DATE: 2000-04-06
'PRIOR PILING DATE: 2000-04-20
'PRIOR FILING DATE: 2000-04-20
'PRIOR APPLICATION NUMBER: 60/200,552
PRIOR PILING DATE: 2000-04-28
'PRIOR PILING DATE: 2000-04-28
'PRIOR PILING DATE: 2000-04-28
'PRIOR PILING DATE: 2000-05-05
'PRIOR FILING DATE: 2000-05-05
'PRIOR FILING DATE: 2000-05-05
'PRIOR FILING DATE: 2000-05-01
'PRIOR FILING DATE: 2000-05-05
'PRIOR FILING DATE: 2000-05-05
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NAME/KRY: misc feature
OTHE INFORMATION: Incyte ID No: 1563237CD1
US-10-257-022-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TANG, Y. Tom
KHAN, Farrah A.
TRIBOULDY, Catherine M.
GANDHI, Ameena R.
YAO, Monique G.
SANJAWALA, Machusudan M.
BAUGHN, Mariah R.
NGUYEN, Danniel B.
                                                                                                                                                                                                                                                                                                                                                                          Sequence 11, Application US/10257022
Publication No. US20030211499A1
GENERAL INFORMATION:
APPLICANT: REDDY, Roopa
APPLICANT: THORNTON, Michael
APPLICANT: BOROWSKY, Mark L.
APPLICANT: TANG, Y. Tom
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APPLICANT:
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TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
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Sequence 766, Application US/10369493

Publication No. US2030233675A1

Sequence 766, Application US/10369493

Publication No. US2030233675A1

APPLICANT: Cao, Yongwei

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

APPLICANT: Glaman, Barry S.

TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES

FILE REFERENCE: 38-10(52052)8

CURRENT FILING DATE: 2003-02-28

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-28

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 766

LENGTH: 490

TENGTH: 490
TITLE OF INVENTION: POLYNUCLECTIDES AND POLYPEPTIDES ASSOCIATED WITH THE NF-KB TITLE OF INVENTION: PATHWAY
FILE REFERENCE: DO284 WP
CURRENT APPLICATION NUMBER: US/10/755,889
CURRENT FILING DATE: 2004-01-13
PRIOR PAPLICATION NUMBER: U.S. 60/440,068
PRIOR APPLICATION NUMBER: U.S. 60/440,757
PRIOR APPLICATION NUMBER: U.S. 60/469,757
PRIOR PILING DATE: 2003-01-14
PRIOR PILING DATE: 2003-01-13
SEQ ID NOS: 823
SEQ ID NO 204
LENGTH: 581
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APPLICANT: Liu, Jingdong
APPLICANT: Liu, Jingdong
APPLICANT: Shou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Gao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(53313)
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Pred. No.
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; Sequence 68020, Application US/10425114
; Publication No. US20040034888A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              258 GSQVSSMLKLAL----QNCCP 274
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1 Similarity 52.6%;
10; Conservative 4
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US-10-369-493-766
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US-10-755-889-204
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Best Local Similarity
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APPLICANT: La Rosa Thomas J
APPLICANT: La Rosa Thomas J
APPLICANT: Avalic David K
APPLICANT: Avalic David K
APPLICANT: Abus
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53223)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT PILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
LENGTH: 338
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Patent No. US20020052308A1

GENERAL INFORMATION:

APPLICANT: ROSE at al.

TITLE OF INVENTION:

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR PRING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE PATENTIN VET: 2.0

SOFTWARE PATENTIN NUMBER: E0/124,270

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SOFTWARE PATENTIN VET: 2.0

SEQ ID NO 1295

LENGTH: 677
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; OTHER INFORMATION: Clone ID: PAT_MRT3847_39039C.1.pep
US-10-424-599-218174
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40.2%; Score 49.5; DB 15;
Best Local Similarity 43.5%; Pred. No. 34;
Matches 10; Conservative 4; Mismatches 4;
                                                                                                                                                                                                                                                                                 DB 15;
                                                                                                                                                                                                   ; OTHER INFORMATION: Clone ID: 700685326_FLI.pep
US-10-425-114-68020
                                                                                                                                                                                                                                                                              Query Match
40.2%; Score 49.5; D
Best Local Similarity 43.5%; Pred. No. 33;
Matches 10; Conservative 4; Mismatches
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 68020
LENGTH: 332
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US-10-424-599-218174
; Sequence 218174, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
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78 GTSVADLLKLLDSDTNASAWPRN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTRISDMLKLI-----ADTWQRN 18
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GTSVADLLKLLDSDTNASAWPRN 94
                                                                                                                              TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Glycine max
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Sequence 33933. Application US/10029386

Publication No. US2030194704A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fent, Starron G.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Hanzel, David R.
APPLICANT: HANCHION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION UNDER: US/10/029,386
CURRENT PILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 33933
LENGTH: 203
LENGTH: 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 38.2%; Score 47; DB 14; Length 203; Best Local Similarity 53.3%; Pred. No. 49; Matches 8; Conservative 1; Mismatches 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: MAP TO ACO05031.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.95
OTHER INFORMATION: SWISSPROT HIT: Q13075, EVALUE 1.00e-112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: November 11, 2004, 02:43:10 Job time : 26.4953 secs
     4 ISDMLKLIADTWORNCCP 21
                                                17 İSGGLKNİSSPFÖRICCP 34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-10-029-386-33933
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Suguence 215390, Application US/10424599
Sublication No. US20040031072A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: AR ROBA Thomas J
APPLICANT: Car Youngwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION NUMBER: US/10/424,599
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684.
SEQ ID NO 215390
LENGTH: 61
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COTER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (161) OTHER INFORMATION: (161) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-925-301-1295
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/10080943

Sequence 4, Application US/10080943

Publication No. US20030073236A1

GENERAL INFORMATION:

APPLICANT: Tsai, Shih-Chong

TITLE OF INVENTION: PL93 PROTEINS AND NUCLEIC ACIDS, AND USES THEREOF

FILE REFERENCE: IU99-PC7

CURRENT APPLICATION NUMBER: US/10/080,943

CURRENT FILING DATE: 2002-10-09

PRIOR PILING DATE: 1999-08-23

NUMBER OF SEQ ID NOS: 4

SOFTWARE Patentin Ver: 2.1

SEQ ID NO 4

LINCTH: 1698
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                                                                                                                                                                                  Length 677;
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US-10-424-599-215390
                                                                                                                                                                             Score 48; DB 9; I
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                5; Mismatches
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1582 GLHIDQLVCLVLEAWQKGPCP 1602
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                                                                                                                                                                                                                                                                                    1 GTRISDMLKLIADTWQRNCCP 21
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Best Local Similarity 33.3%;
Matches 7; Conservative
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Matches 7; Conservative
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Matches 10, Conservative
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ORGANISM: Glycine max
FEATURE:
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US-10-080-943-4
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November 10, 2004, 13:40:53 ; Search time 5.39623 Seconds (without alignments) 392.268 Million cell updates/sec Run on:

US-10-092-750-54 123 1 GTRISDMLKLIADTWQRNCCPA 22 Title: Perfect score: Sequence:

283416 segs, 96216763 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR 79:*
1: pir1:*
2: pir2:*
3: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		ф				
Result		Query				
No.	Score	Match	Length	B	-	Description
	50	40.7	490		JC6038	probable molybdenu
73	20	40.7	490	7	D90727	hypothetical prote
ო	20	0	491	~	AH0594	~
4	20	ö	494	7	E85578	hypothetical prote
ιΩ	4	39.8	329	7	D69494	
9	48	Φ	418	Ŋ	F96790	hypothetical prote
7	48	σ	732	~	T43619	
60	48	39.0	732	N	830060	protein kinase ypk
o,	48	σ	810	Ŋ	T33323	hypothetical prote
10	47.5	38.6	3947	N	T52486	ໝ
11	47	œ	498	ď	DS9093	hypothetical prote
12	47	α	517	N	D86264	Н
13	47	38.2	1232	N	A55478	neuronal apoptosis
14	47	æ	1447	N	T42628	neuronal apoptosis
15	46	$\sim$	495	N	T27936	hypothetical prote
16	46	37.4	636	~	T10569	probable serine/th
17	46	۲.	2330	Н	RRIWMV	genome polyprotein
	44	S	127	7	146269	
	44	Ŋ	178	7	S74871	transposase slr124
	44	35.8	227	N	T04420	ribonuclease (EC 3
21	44	5	267	7	T22978	hypothetical prote
	44	'n.	474	7	B46746	glycine hydroxymet
	44	ď.	475	N	A33696	glycine hydroxymet
	44	īŪ,	1116	N	S77213	DNA-directed DNA p
	44	5	1220	(7)	AD0125	exodeoxyribonuclea
	44	'n.	2476	7	T34022	zonadhesin - pig
	43	'n.	σ	7	B95323	_
28	43	35.0	334	7	A70101	$\overline{}$
29	43	υ.	377	7	AD2922	altronate oxidored

altronate oxidored	procein rycib.29 ( hypothetical prote	hypothetical prote hypothetical prote	н	hypothetical prote	hypothetical prote	hypothetical prote	HMG-1 protein homo	protein T20M3.4 [i	hypothetical prote	hypothetical prote	scyllo-inosamine-4	probable arginase	glyceraldehyde-3-p
E97696	796504 716846	T15119 S69557	RUPSEO	T51912	A64435	AF1880	A41302	C86192	T36382	H64488	XJSMIG	T13422	B24430
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35.0	35.0	35.0	34.6	34.6	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1	34.1
4. w.	4 4 8 8	44 43	42.5	42.5	42	42	42	42	42	42	42	42	42
`0 °	31 32	33	32		37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1 JC6038 probable molybdenum transport protein modF - Escherichia coli (strain K-12) N,Alternate names: photorepair protein phrA
C;Species: Escherichia coli C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: JC6038; H64811; T56601; S32737 C;Accession: W : Part P M : Part I T : Holly P C : Chanmidam V T
, snammugam, lybdate trans
A;Reference number: JC6037; MJD:96146523; PMID:8550508 A;Accession: JC6038 A;Molecule type: DNA
A;Residues: 1-490 <gru> A;Cross-references: UNIPROT:P31060; GB:U27192; NID:g973213; PID:g973219 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C</gru>
.A.; Kose, D.L.; Mau, B.; Shao, I. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichia coli K-12. A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: H64811 A;Status: nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
A,Residues: 1-490 <blat> A,Residues: 1-490 <bb.ae000178; a,experimental="" gb.u00096;="" k-12,="" mg1655<="" nid:g1786967;="" pid:g178697e="" pidn.aac73847.1;="" source:="" strain="" substrain="" td=""></bb.ae000178;></blat>
R;Dorrell, N.; Ahmed, A.H.; Moss, S.H. Photochem. Photobiol. 58, 831-835, 1993 A.Title: Photocactivation in a phrB mutant of Escherichia coli K-12: evidence for the
A;Accession: 160601 A;Status: preliminary; translated from GB/EMBL/DDBJ
AA y,'A',321,'R',323-324,'A',326-490 <res> : EMBL:X69182; NID:g296334; PIDN:CAA48926.1; PID:g296235 roe: K-12 strain C600; cell line JM83/pND01</res>
C;Genetics: A;Gene. Map modf; phrA A;Map position: 17 min C;Superfamily: Escherichia coli probable molybdenum transport protein modf; ATP-binding C;Keywords: ATP; DNA repair; GTP binding; nucleotide binding; P-loop; transport proteir E;19-211/Domann: ATP-binding cassette homology cABCl> F;36-43/Region: nucleotide-binding motif A (P-loop) F;276-479/Domain: ATP-binding cassette homology cABC2> F;293-300/Region: nucleotide-binding motif A (P-loop)
Query Match Best Local Similarity 52.6%; Pred. No. 6.8; Matches 10; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

2 TRIS--DMLKLIADTWQRN 18

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1,

Gaps

5

Indels

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2-hydroxyglutaryl-CoA dehydratase, subunit beta (hgdB) homolog - Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus fulgidus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: Archaeoglobus C;Species: 
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C;Superfamily: Escherichia coli probable molybdenum transport protein modF; ATP-binding
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C;Superfamily: 2-hydroxyglutaryl-CoA dehydratase beta chain
                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-94 <5TO:
A;Cross-references: UNIRROT:08X941; GB.AE005174; NID:g12513692; PIDN:AAG55089.1; GSPDB:
A;Experimental source: strain 0157:H7, substrain EDL933
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                            A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: E85578
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Pred. No. 6.9;
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Pred. No. 6
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TRLSFEQLQKLVSDEWQRN 90
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Best Local Similarity 52.6%;
Matches 10; Conservative 4
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llarity 52.9%;
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A,Molecule type: DNA
A,Residues: 1-418 <STO>
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Nature 413, 848-852, 2001
A;Althors: Parry, C.; Quiai, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Althors: Parry, C.; Quiai, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; A;Althors: Parry, C.; Quiai, M.; Rutherford, M.; Parrar, A;Roference number: AB0504
A;Accession: AH0594
A;Accession: AH0594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-491 < PAR>
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.Cross-references: GB:AL513382; PIDN:CAD05226.1; PID:g16501996; GSPDB:GN00176
                                                                                                                                                                                                                                                   hypothetical protein ECs0788 [imported] - Escherichia coli (strain O157:H7,
                                                                                                                                                                                                                                                                                                                      Species: Escherichia coli
;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
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TRLSFEQLOKLVSDEWORN 86
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Best Local Similarity
Matches 10; Conserv
89
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Clacesion: 15486
R;Gentil, G.; Yuan, M.W.; Budde, A.D.; Dohren von, H.; Leong, S.A.
Bubmirted to the EMBL Data Library, July 1996
A;Description: Characterization of the Ustilago maydis sid2 gene encoding a multidomair synthetic pathway.
A;Reference number: 226091
A;Accession: T55486
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Mccession: 15947 cGEN>
A;Residues: 1-3947 cGEN>
A;Cross-references: UNIPROT:043103; EMBL:U62738; NID:g2731632; PID:g2731633; PIDN:AAB91
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,Accession: T33323
A,Status: preliminary; translated from GB/EMBL/DDBJ.
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-810 < UDUZ>
A,Cross-references: UNIPROT:Q9TZQ4; EMBL:AF077529; PIDN:AAC26255.1; GSPDB:GN00020; CESP
A,Experimental source: strain Bristol N2; clone C09E8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,Map position: 2
A,Introns: 30/2; 70/1; 118/3; 149/2; 167/3; 293/3; 337/3; 406/3; 449/3; 480/1; 525/3; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ajgene: sid2
C;Superfamily: non-ribosomal peptide synthetase
C;Superfamily: non-ribosomal peptide synthetase
C;Superfamily: non-ribosomal peptide synthetase
C;Superfamily: non-ribosomal phosphopantetherin; phosphoprotein
F;303-771/Domain: acetate-CoA ligase homology <ACL1>
F;801-870/Domain: acetate-CoA ligase homology <ACL2>
F;2540-2991/Domain: acetate-CoA ligase homology <ACL2>
F;3020-3089/Domain: acetate-CoA ligase homology <ACL2>
F;3054,3611/Binding site: phosphopantetheine (Ser) (covalent) #status predicted
                                                                                                                                                                                                                                                     hypothetical protein C09E8.1 - Caenorhabditis elegans C5Species: Caenorhabditis elegans C5Species: Caenorhabditis elegans C5Species: Caenorhabditis elegans C5Accession: T3323 R5Du, Z.; Graves, T.; Gibson, A. R5Du, Z.; Graves, T.; Gibson, A. A. Species: C6 the RMEL Data Library, July 1998 A; Reference number: Z21322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ferrichrome siderophore peptide synthetase - smut fungus (Ustilago maydis)
C,Species: Ustilago maydis (corn smut)
C,Date: 24-Oct-2000 #sequence_revision 24-Oct-2000 #text_change 12-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3947;
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Pred. No. 22;
6; Mismatches 7; Indels
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                              Indels
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llarity 35.0%; Pred. No. 1.2e+02;
Conservative 7; Mismatches 3;
  ed. No. 20;
Mismatches
        Pred. No.
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                                                                                                                                 219 GWRCSDTLRTLADSWKQ 235
                                                                               1 GTRISDMLKLIADTWQR 17
Best Local Similarity 47.1%;
Matches 8; Conservative !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 35.0%;
Matches 7; Conservative
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Best Local Similarity
Matches 7; Conserv
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A;Gene: CESP:C09E8.1
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A;Cross-references: UNIPROT:Q9SFW6; GB:AE005173; NID:g6554487; PIDN:AAF16669.1; GSPDB:GN C;Genetics:
C;Genetics:
A;Gene: F15M4.19
A;Map position: 1
C;Superfamily: cyclin, A/B/D/E type
                                                                                                                                                                                                                                                                                                                                                                                                                                           secreted protein kinase ypkA - Yersinia pestis plasmid pcD1
NyAlternate names: protein kinase A homolog
CiSpecies: Yersinia pestis
Cjacies: Yersinia pestis
Cjacies: 1-3n-12000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
CjAciesion: T43619; T42850
RiHu, P.; Elliott, J.; McCready, P.; Skowronski, E.; Garnes, J.; Kobayashi, A.; Brubaker
A; Title: Structural organization of virulence-associated plasmids of Yersinia pestis.
A; Reference number: 222578; MUID: 98422474; PMID: 9748454
A; Accession: T43619
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A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-732 <GLD
A,Cross-references: UNIPROT:Q05608; EMBL:X69439; NID:g49186; PIDN:CAA49215.1; PID:g49187
C;Keywords: serine/threonine-specific protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>'</u>
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C. Jate. 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C. Accession: 830060
R. Galyov, E.E.; Hakansson, S.; Forsberg, A.; Wolf-Watz, H.
Nature. 361, 730-732, 1993
A.; Tille: A secreted protein kinase of Yersinia pseudotuberculosis is an indispensable A. Reference number: 830060; MUID:93180911; PMID:8441468
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A;Molecule type: DNA
A;Residues: 1-732 <PER>A;Residues: 1-732 <PER>A;Coss-references: EMBL:AF074612; NID:g3822037; PIDN:AAC69765.1; PID:g3822045
A;Experimental source: strain KIM5
C;Genetics:
                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                  Length 418;
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                                                                                                                                                                                                                 Indels
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Pred. No. 20;
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                                                                                                                                                               Score 48; DB Pred. No. 12; 2; Mismatches
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                                                                                                                                                                                                                                                                                                                    276 TEILDMEKLMANTLOFNFC 294
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nilarity 47.1%; I
Conservative 5;
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Best Local Similarity 57.9%;
Matches 11; Conservative
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Best Local Similarity
Matches 8; Conserv
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A;Genome: plasmid pCD1
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Length 732;

39.0%; Score 48; DB 2;

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A,Gene: GDB:SMA@; SWA
A,Cross-references: GDB:120378; CMIM:600354; CMIM:253300
A,Cross-references: GDB:120378; CMIM:600354; CMIM:253300
A,Cross-references: GDB:120378; CMIM:600354; CMIM:253500
C;Keywords: apoptosis: ATP; Glycoprotein; nucleotide binding; P-loop; transmembrane #status predicted <TWM1>
F;940-410/Domain: transmembrane #status predicted <TWM2>
F;470-46/Domain: transmembrane #status predicted <TWM2>
F;470-86/Domain: predicted F;618,632,923,1035/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A, Cross-references: UNIPROT: Q9QUK4; EMBL: AF102871; NID: 93860228; PID: 93860229; PIDN: AAC, Genetics:
R;Roy, N.; Mahadevan, M.S.; McLean, M.; Shutler, G.; Yaraghi, Z.; Farahani, R.; B d, T.O.; de Jong, P.J.; Surh, L.; Ikeda, J.E.; Korneluk, R.G.; MacKenzie, A. A.C.11 80, 167-178, 1995
A;Title: The gene for neuronal apoptosis inhibitory protein is partially deleted A;Reference number: A55478; MUID:95112344; PMID:7813013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Nolecule type: DNA
A;Residues: 1-455 cLEI
A;Cross-references: UNIPROT:023552; EMBL:U39998; PIDN:AAA81102.1; CESP:ZK622.3
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T27936
R;Leimbach, D.
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A; Description: The sequence of C. elegans cosmid ZK622.
A; Reference number: Z20443
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Pred. No. 4
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Best Local Similarity 53.37
Best Local 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               479 LLKKIAFLWASGCCP
                                                                                                                                                                                                                                           A,Molecule type: mRNA
A,Residues: 1-1232 <ROY>
A,Cross-references: GB:U19251
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Best Local Similarity
Matches 9; Conserv
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chinologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Coundy, A.R.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C. C.A.; Li, U.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. B.; Southwick, A.M.; Sun, H.; Tallon, kar, W. W. D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Recence number: A66141; MUID:21016719; PMID:11130712
A;Residues: D1577
A;Residues: L-517 <STO>
A;Cross-references: UNIPROT:Q9SAD9; GB:AE005172; NID:g4850387; PIDN:AAD31057.1; GSPDB:GN
                                                                                                                                                                                                                                                                                                                                     A,Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori A,Title: Sequence and organization of pXO1, the large Bacillus anthracis plasmid harbori A,Reference number: AS9091, MUID:99445483; PMID:10515943
A,Accession: D59093
A,Status: pression: D59093
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A,Molecule type: DNA
A,Residues: 1-498 < OKI>
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                                                                                                                              hypothetical protein pXO1-20 - Bacillus anthracis virulence plasmid pXO1 C; Species: Bacillus anthracis C; Dactes: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004 C; Accession: D59093 R; Oklinaka, R.T.; Cloud, K.; Hampton, O.; Hoffmaster, A.R.; Hill, K.K.; Keim, J. Bacteriol. 181, 6509-6515, 1999
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N'Alternate names: NAIP
C'Species: Homo sapiens (man)
C'Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 02-Feb-2001
C'Accession: A55478
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A;Genome: plasmid
C;Superfamily: Bacillus anthracis plasmid pXO1 hypothetical protein
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Pred. No. 21;
5; Mismatches 7; Indels
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Pred. No. 20;
2; Mismatches 1; Indels
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Best Local Similarity 72.7%;
Matches 8; Conservative
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ilarity 36.8%;
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A;Map position:
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RESULT 13 A55478

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A,Introns: 34/2; 97/2; 222/3; 310/3 C;Superfamily: Caenorhabditis elegans hypothetical protein ZK622.3
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Query Match
37.4%; Score 46; DB 2; Length 495;
Best Local Similarity 43.8%; Pred. No. 29;
Matches 7; Conservative 6; Mismatches 3; Indels 1 GTRISDMIKLIADTWQ 16 || :::::|| :||| 275 GTSFNELVELIKNTWQ 290 ò

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Search completed: November 10, 2004, 14:52:22 Job time : 6.39623 secs

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Gapop 10.0 , Gapext 0.5
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Q6d884 erwinia car
Q7plm6 drosophila
Q9x2z1 bacillus an
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Az12g770 bacillus
Q96d10 homo sapien
Q66210 yersinia en
Q65239 yersinia en
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Q8747 mus musculu
Q8tdz4 homo sapien
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TISSUE=Blood;
MEDLINE=2288257; PubMed=12477932;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver;
MEDLINE=21293069; PubMed=11283018;
Hammond P.W., Alpin J., Rise C.B., Wright M., Kreider B.L.;
Hammond P.W. Alpin J., Rise C.B., Wright M., Kreider B.L.;
HIN Vitro Selection and Characterization of Bcl-Xx-binding Proteins
from a Mix of Tissue-specific mRNA Display Libraries.";
J. Biol. Chem. 276:20898-20906(2001).

EMBL: AR357524; AAK60628.1;
                                                                                                                                                                                                                                                                                                                                                                    096JA9;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Bcl-XL-binding protein t25 (Fragment).
Bcl-XL-binding protein t25 (Fragment).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarxhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCEL TaxID=9606;
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Solute carrier family 15, member 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          581 AA.
                                                                                                                                                                                                                                                                                                                                                    22 AA.
                                                                                                                                                                                                                                                                     ALIGNMENTS
   Q6D884
Q7PLM6
Q7CMJ4
Q9XZZI
AAT28770
Q9SAQ2
CGP2 HUMAN
Q56921
Q85239
Q93KQ6
CUL7 MOUSE
Q8TDZ4
Q8CH71
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Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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       3997
44998
44998
7017
7028
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       NCBI_TaxID=9606;
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005608 Versinia ps 09t2d caenorhabdi 0614b3 solanum dem Aat40504 solanum d 014999 home sapien 043103 ustilago ma 0813w4 mus musculu

Q61fm7 plasmodium Cag25209 plasmodiu

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STRAIN=PEST
                                                                                                                                                  Name=arsR;
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                                                                            Q9RA93;
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Matches
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Q7Q0F9
                                  RESULT 4
                                              09RA93
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Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Caravant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Tochiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Halton E., Ketreman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Anders S.J., Marra M.A.,
Jones S.J., Marra M.A.,
T. "Generation and initial analysis of more than 15,000 full-length human for the mouse cDNA sequences.",
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
41.5%; Score 51; DB 2; Length 581;
Best Local Similarity 47.6%; Pred. No. 22;
Matches 10; Conservative 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                         TISSUE-Blood;
Strauberg R.;
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037974; AAH37974.1; -.
Genew; HGNC:18068; SLC15A3.
GO; GO:0016620; C:membrane; IEA.
GO; GO:0005215; P:transporter activity; IEA.
GO; GO:0005857; P:clansporter activity; IEA.
InterPro; IPR000109; PTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Flacenta;
Ishiabshi K., Imai M.;
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AB020599; BAA93432.1; -
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005215; F:transporter activity; IEA.
GO; GO:006857; P:oligopeptide transport; IEA.
InterPro; IPRO(199; PTR2.
                                                                                                                                                                                                                                                                                                                                                                                                                     63593 MW; 6E2BF8FE39F3B15E CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide transporter 3.
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SEQUENCE 581 AA; 6
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Q9P2X9
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258 GSQVSSMLKLAL --- ONCCP 274

S 8

1 GTRISDMLKLIADTWQRNCCP 21

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Anophales gambiae str. PEST.
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptora; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
NCBI_TaxID=180454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                          STRAIN=A84;

Xu Z.Q., Zhang R.;

Xu Z.Q., Zhang R.;

Xu Z.Q., Zhang R.;

Submitted (4002-1999) to the EMBL/GenBank/DDBJ databases.

-!- SIMILARITY: Contains 1 HTH arsR-type DNA-binding domain.

EMBL; AF10758; AAD51845-1;

GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003750; F:transcription factor activity; IEA.

GO; GO:000315; P:regulation of transcription, DNA-dependent; IEA.

InterPro; IPRO01945; HTH ArsR.

InterPro; IPRO01958; Wing-hix_DNA_bnd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anopheles Genome Sequencing Consortium;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
preliminary data.
EMBL, AAAB01008985; EAA15174.1; -.
SEQUENCE 444 AA; 51316 MW; B459837EIF270951 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.1%; Score 50.5; DB 2; Length 115; 39.3%; Pred. No. 5.1; ive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 41.1%; Score 50.5; DB 2; Length 444; Local Similarity 50.0%; Pred. No. 20; es 12; Conservative 3; Mismatches 2; Indels 7
                                                                                                                                                                  Sinorhizobium sp. As4.
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00778; HTHARSR.
SMART; SM00418; HTH. ARSR; 1.
DNA-binding; Transcription regulation.
SEQUENCE 115 AA; 13304 MW; B63B3D6E41EB3F46 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-WAR-2004 (TrEMBLrel. 26, Created)
01-WAR-2004 (TrEMBLrel. 26, Last sequence update)
01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                              Last sequence update)
Last annotation update)
  115 AA.
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TRVSQLLKLLGDKTRLTIVSILKQRECC 36
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                                                  13,
13,
26,
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Best Local Similarity 39.3
Matches 11, Conservative
PRELIMINARY;
                                                                           01-MAY-2000 (TrEMBLrel.
01-MAR-2004 (TrEMBLrel.
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                                               01-MAY-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrembLrel. 27, Last annotation update)
Protein tyrosine phosphatase.
Cotesia glomerata polydnavirus.
Viruses; dsDNA viruses, no RNA stage; Polydnaviridae; Bracovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Cerutti P., Duonor-Cerutti M., Devauchelle G.;
"Full-length protein tyrosine phosphatase from a genomic bank of
"Full-length protein tyrosine phosphatase from a genomic bank of
"Cotesia a Qlomerata bracovirus.";
Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; AY466396; AAR29979.1;
FONTENCE 314 AA; 36583 MW; 5B0EBCB9E71A42D6 CRC64;
                                                                                                               Viruses; dsDNA viruses, no RNA stage; Polydnaviridae; Bracovirus.
NCBI_TaxID=257816;
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SEQUENCE FROM N.A.

Ceruttia (NOV-2003) to the EMBL/GenBank/DDBJ databases.

L. Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.

R. DEFPRON 1 PR003895; PTPC—Morif.

R. InterPro; IPR000381; TYR_phosphatase.

R. InterPro; IPR000381; TYR_phosphatase.

R. Fram; PF00102; Y_phosphatase.

R. SMART; SM00194; PTPC; 1.

R. SMART; SM00404; PTPC; 1.

R. SMART; SM00404; PTPC—Morif; 1.

R. PROSITE; PS00383; TYR_PHOSPHATASE 1; 1.

R. PROSITE; PS00383; TYR_PHOSPHATASE 2; 1.
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45.0%; Pred. No. 17;
ive 3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 50; DB 2; Length 314;
Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                 314 AA; 36583 MW; 5B0EBCB9E71A42D6 CRC64;
                                                                     05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Protein tyrosine phosphatase.
Cotesia glomerata polydnavirus.
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                               314 AA
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                                                            Created)
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                               PRELIMINARY;
                                                           (TrEMBLrel.
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Best Local Similarity
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les 9; Conserv
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MODF_ECOLI
ID MODF_ECOLI
AC P31060;
                                           0684V0;
05-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                     Hydrolase.
SEQUENCE
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                                Q6S4V0
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Matches
RESULT 6
Q6S4V0
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=KI2 / (5600;

MEDLINE=94143420; PubMed=8310005;

DOTTELL N., Ahmed A.H., Moss S.H.;

DOTTELL N., Ahmed A.H., Moss S.H.;

"Photoreactivation in a phrB mutant of Escherichia coli K-12: evidence for the role of a second protein in photorepair.";

Photochem. Photobiol. 58:831-835(1933).

-! FUNCTION: Involved in the transport of molybdenum into the cell.

Involved in photorepair. Could act on UV-induced DNA damage other than pyrimiddine dimers.

-! SUBCELLULAR LOCATION: Inner membrane associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mamira S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Sampei G., Seki Y., Tagami H., Takemoto H., Nishio Y., Saito M., Yano M., Horiuchi T.;

"A 718-kb DNA sequence of the Escherichia coli K-12 genome corresponding to the 12.7-28.0 min region on the linkage map.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=9742667; PubMed=9278503; MEDLINE=97426677; PubMed=9278503; MEDLINE=97426677; PubMed=9278503; MEDLINE=97426677; PubMet G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.; Man B., Shao Y.; Man B., Shao Y.; Science 277:1453-1474(1997).
01-JUL-1993 (Rel. 26, Created)
1-OCT-1995 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Putative molybdenum transport ATP-binding protein mod? (Photorepair
                                                                                                                             Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
NCBI_TaxID=562;
                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAINEALS / MOLD00;
MREDINE-86151473; PubMed-8564363;
Walkenhorst H.M., Hemschemeier S.K., Eichenlaub R.;
"Mollecular analyysis of the molybdate uptake operon, modABCD,
"Escherichia coli and modR, a regulatory gene.";
Microbiol. Res. 150:347-361(1995).
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=K12; Shanmugam K.T.; Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Belongs to the ABC transporter family.
                                                                                             Synonyms=phrA; OrderedLocusNames=b0760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12;
MEDLINE=97061202; PubMed=8905232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U27192; AAB60176.1; -. AE000178; AAC73847.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U07867; AAB06891.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D90714; BAA35422.1; -. D90715; BAA35424.1; -.
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                      Escherichia coli
                                                                                protein phrA)
Name=modF; Sy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
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490 AA

PRT;

68 TRLSFEQLOKLVSDEWQRN 86

EMBL; X69182; CAA48926.1; -.

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Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Name=modF; Ordered!
Shigella flexneri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shigella flexneri
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ATP-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                       Q7C2Q7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q83M03
                                                                              RESULT 10
Q7C2Q7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
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SEQUENCE FROM N.A.

RESTAIN-0157:H7 / RIMD 0509952 / EHEC;

X MEDLINE-21156231; PubMed=11258796;

X HAYASH, T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA HAYASH, T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA HAN C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Panaka M., Shinagawa H.;

RA HAN C.-G., Ohtsubo E., Nakayama K., Murata T., Panaka M., Shinagawa H.;

RA HAN C.-G., Ohtsubo E., Nakayama K., Murata T., Panaka M., Shinagawa H.;

RO JOSSES BABB42111, -

RE MEBL, APOOSSES, BABB42111, -

RE MEBL, APOOSSES, BABB42111, -

RE MEBL, APOOSSES, BABB42111, -

RE MEBL, APOOSSES, BABB42111, -

RE MEBL, APOOSSES, BARG Lransporter.

RE MER MEDLONOSSES, ABG Lransporter.

RE MEMRY, SWOOSSES, ABG Lransporter; 2.

RE MEMRY, SWOOSSES, ABA, Z.

RE MEMRY, SWOOSSES, ABA, Z.

RE MEMRY, SWOOSSES, ABA, Z.

RE MEMRY, SWOOSSES, ABA, Z.

RE MEMRY, SWOOSSES, ABA, Z.

RE MEMRY, SWOOSSES, ABA, Z.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
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7
                                                                                                                                                                                                                                              PROSITE; PS00211; ABC_TRANSPORTER 1; FALSE_NEG.
PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
ATF-binding; Complete proteome; DNA repair; Inner membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40.7%; Score 50; DB 2; Length 490; 52.6%; Pred. No. 27; tive 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 L -> A (in Ref. 5).
G -> R (in Ref. 5).
R -> A (in Ref. 5).
; 97C220824ED66FB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 AA; 54479 MW; F7569D0284D1E1C5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-binding component of molybdate transport system.
0rderedLousNames=ECS0788;
                                                                                                                                                                                                                                                                                                                                                                 ABC transporter 1.
ABC transporter 2.
ATP (Potential).
ATP (Potential).
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               PIR, JC6038, JC6038.
Echobas: BB1628; --
EcoGene: BG11677; mcdF.
InterPro; IPR003539; AAA ATPase.
InterPro; IPR003439; AAC transporter.
Pram; PP000005; ABC trans. 2.
Probom; PD000006; ABC transporter; 2.
SWART; SM00382; AAA; Z.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 50;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ||:| : ||:| 68 TRLSFEQLQKLVSDEWQRN 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 TRIS--DMLKLIADTWORN 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54535 MW;
                                                                                                                                                                                                                                                                                                                                         Molybdenum; Repeat; Transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40.7%;
Local Similarity 52.6%;
hes 10; Conservative 4
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Best Local Similarity 52.6
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                       320
322
325
325
390 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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Matches
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RADOR REPERENCE OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTION OF STREET SOLUTI
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2 TRIS--DMLKLIADTWQRN 18

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"Genome sequence of Shigella flexneri 2a: insights into pathogenicity through comparison with genomes of Escherichia coli K12 and O157."; Nucleic Acids Res. 30:4432-4441(2002).
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STRAIN=301 / Sertytype 2a,
MEDIAIN=32272406; PubMed=12384590,
Jin O., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
Sun L., Xue Y., Zhao A. (Sao Y., Zhu J., Kan B., Ding K., Chen S.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

STRAIN-2457T;

MEDLINE-2259074; PubMed=12704152;

MEDLINE-2259074; PubMed=12704152;

MEDLINE-2259074; PubMed=12704152;

Medi J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,

A Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,

Schwartz D.C., Blattner F.R.;

I "Complete genome sequence and comparative genomics of Shigella

I flexner; serotype 2a strain 2457T,";

Infect. Immun. 71:273-2786(2003).

-! SIMILARITY: Belongs to the ABC transporter family.

R EMBL; AE016979; AAP16661.;

R GO; GO:0005524; F:ATP binding; IEA.

R InterPro; IPR003533; AAA-ATPASS.

R InterPro; IPR003533; AAA-ATPASS.

R InterPro; IPR003533; AAA-ATPASS.
                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                      Darling A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
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52.6%; Pred. No. 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     490 AA; 54656 MW; ECE2582DF62827AE CRC64;
05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ATP-binding component of molybdate transport system.
Name=modFi_OrderedLocusNames=80552;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-UTN-2003 (TrEMBLrel. 24, Created)
01-UTN-2003 (TrEMBLrel. 24, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-binding component of molybdate transport system.
Name=modf; OrderedLocusNames=SP0544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               490 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50893; ABC_TRANSPORTER_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00005; ABC tran; 2.
ProDom; PD000006; ABC transporter; 2.
SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Gaps

5

Indels

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Length 491;

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PROSITE; PSS0893; ABC_TRANSPORTER_2; 2.
ATP-binding; Complete proteome.
SEQUENCE 491 AA; 54745 MW; 3A0FCD9460785F39 CRC64;
                                                                                                                                                                                              Query Match
40.7%; Score 50; DB
Best Local Similarity 52.6%; Pred. No. 27;
Matches 10; Conservative 4; Mismatches
Pfam; PP00005; ABC tran; 2.
ProDom; PD000006; ABC transporter; 2.
SMART; SM00382; AAA; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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(TrEMBLrel. 23, I
(TrEMBLrel. 26, I
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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hes 10; Conserv
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Matches
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ID Q8
AC Q8
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-!- SIMILARITY: Belongs to the ABC transporter family.
-!- SIMILARITY: Belongs to the ABC transporter family.
BMBL; AL627268 CAD05226.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:000166; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
GO; GO:000166; P:nucleotide binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkhill J., Dougan G., Janes K.D., Thomson N.R., Pickard D., Wain J., Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M., Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Daviss R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Quail M.A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Simmonds M., Skelton J., Stevens K., Mitchead S., Barrell B.G.; a multiple drug resistant Salmonella enterica servovar Typhi CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.,
"Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
and CI18.";
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01-NAR-2002 (TrEMBLrel. 20, Last sequence update)
01-0CT-2004 (TrEMBLrel. 28, Last annotation update)
Putative_molybdenum transport ATP-binding protein ModF (Photorepair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=modf; OrderedLocusNames=STY0811, t2109;
Salmonella typhia
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceee; Salmonella.
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to the ABC transporter family
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InterPro; IPR003439; ABC_transporter.
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STRAIN-TY2 / ATCC 700931;
MEDLINE-22531367; PubMed=12644504;
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68 TRLSFEQLQKLVSDEWQRN 86
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Matches 10; Conservative
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-!- SIMILARITY: Belongs
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STRAIN=LT2;
MEDLINE=21534948; PubMed=11677609;
MEDLINE=21534948; PubMed=11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille F.,
Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
Ryan E., Sun H., Florae L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
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                                                                                                                                                                                                                                                Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 413:852-856(2001).

-!- SIMILARITY: Belongs to the ABC transporter family.
-!- SIMILARITY: Belongs to the ABC transporter family.
-!- SGO016020; AAL19716.1; -.-
GO; GO:0005524; F:ATP binding cassette (ABC) transporter acti.
GO; GO:0000166; F:ATP-binding cassette (ABC) transporter acti.
GO; GO:0000166; F:ATP-binding cassette (ABC) transporter acti.
GO; GO:0000166; F:ATP-binding cassette (ABC) transporter acti.
InterPro; IPR003393; AAA APPasse.
InterPro; IPR003499; ABC_transporter.
Ffam; PP00005; ABC_transporter.
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                              QBZQR9;
01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Putative ABC superfamily (Atp. bind), molybdenum transporter.
Name=modF; OrderedLocusNames=STM0778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.7%; Score 50; DB 2; Length 491; 52.6%; Pred. No. 27;
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491 AA; 54696 MW; F25160AA27043BDD CRC64;
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Last sequence update)
Last annotation update)
491 AA.
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SEQUENCE FROM N.A.

STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;

MEDLINE=21074935; PubMed=11206551;

A POSTAIN N.T., Plunket G. III, Burland V., Mau B., Glasner J.D.,

A Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

A POSTAI G., Hackett G., Klink S., Boutin A., Shao Y., Miller L.,

A Grotbeck E.J., Davis N.W., Lin A., Dimilanta E.T., Potanousis K.,

A Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

A Moclor R.A., Blattner F.R.,

I "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

L Nature 409:529-533(2001).

C SIMILARITY: Belongs to the ABC transporter family.

E MEL, AE005254; AAG55089:1;

R PIR; D80727; D90727.

PIR; PIR; E85578;
                                                                                                                                                            STRAIN=06:HI / CFT073 / ATCC 700928;
MEDLINE=22388234; PubMed=12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
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01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 20, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
ATP-binding monoment of molybdate transport system.
Name=modR; OrderediocusNames=20930;
Bacherichia coli 0157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriacee; Escherichia.
                                                               Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
                                                                                                                                                                                                                                                                                                        of uropathogenic Escherichia coll.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024 (2002).

-! SINILARITY: Belongs to the ABC transporter family.

EMBL, AE016757, AAN/9309.1, -.

GO, GO:0016020; C:membrane; IEA.

GO, GO:000524; F:ATP binding; IEA.

GO, GO:0000166; F:ATP-binding cassette (ABC) transporter acti.

GO, GO:0000166; F:ATP-binding cassette (ABC) transporter acti.

InterPro; IPR003593; AAA ATPase.

InterPro; IPR003593; AAA ATPase.

InterPro; IPR000005; HTHAzaC.
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7
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40.7%; Score 50; DB 2; Length 494;
Best Local Similarity 52.6%; Pred. No. 27;
Matches 10; Conservative 4; Mismatches 3; Indels
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Pfam; PP00005; ABC_tran; 2.
SPCDOm; PD000006; ABC_transporter; 2.
SMART; SM00382; AAA; Z.
PROSITE; PS0093; ABC_TRANSPORTER_2; 2.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
ATP-binding; Complete_proteome.
ATP-binding; Complete_proteome.
ATP-binding; Complete_proteome.
ATP-binding; Complete_proteome.
ATP-binding; Complete_proteome.
Putative molybdenum transport ATP-binding protein modF.
Name=modF; OrderedLocusNames=c0836;
Escherichia coli 06.
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                                                                              Enterobacteriaceae; Escherichia.
NCBI_TaxID=217992;
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Q8X941
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DR GO; GO:0016020; C:membrane; IEA.

DR GO; GO:0005524; F:ATP binding; IEA.

DR GO; GO:0004009; F:ATP-binding casecte (ABC) transporter acti. . .; IEA.

DR GO; GO:000166; F:muclectide binding; IEA.

DR GO; GO:0000166; F:muclectide binding; IEA.

DR InterPro; IPR003439; AAA ATPase.

DR InterPro; IPR003439; AABC_transporter.

DR Pfam; PF000000; ABC_transporter.

DR PROSITE; PS50893; ABC_TRANSPORTER_2; 2.

KW ATP-binding; Complete proteome.

SQUERY MAtCh

Query Match

Query Match

A17%; Score 50; DB 2; Length 494;

Best Local Similarity 52.6%; Pred. No. 27;

Matches 10; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Cy 2 TRIS--DMIKLIADTWQRN 18

Db 72 TRLSFEQLOKLYSDEWQRN 90

Search completed: November 10, 2004, 14:50:18

Job time : 31.3057 secs
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